

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 30, 2003, 16:35:33 ; Search time 5937.36 Seconds
(without alignments)
12661.132 Million cell updates/sec

Title: US-09-856-681-1

Sequence: 3093
1 atcaggtcaggaagccttgc.....ccatgatgcgtctacataa 3093

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_estlum:*
3: em_estlin:*
4: em_estmu:*
5: em_estro:*
6: em_estpl:*
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8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
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16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vtl:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vtl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3089.8	99.9	6875	11	BC032619 Homo sapi
2	1439.4	46.5	3226	11	AK042751 Mus muscu
3	1437.6	46.5	3329	11	AK082711 Mus muscu
4	1065.8	34.5	2411	14	CB605722 AMGNNUC:M

5	899.4	29.1	1030	12	BM450002
6	895	29.0	1183	12 <td>BM546059</td>	BM546059
7	828.2	26.8	868	9	A0140366
8	813.8	26.3	891	13 <td>B0186963</td>	B0186963
9	784.4	25.4	887	12 <td>BG769297</td>	BG769297
10	783.4	25.3	1201	9	AL543344
11	779.4	25.2	848	13 <td>B0678536</td>	B0678536
12	772.4	25.0	883	13 <td>B0172225</td>	B0172225
13	770	24.9	864	13 <td>B0440312</td>	B0440312
14	767.4	24.8	874	13 <td>B0838082</td>	B0838082
15	760.6	24.6	890	13 <td>B0683009</td>	B0683009
16	757.4	24.5	953	13 <td>B0854884</td>	B0854884
17	734	23.7	952	13 <td>B0855855</td>	B0855855
18	713.8	23.1	835	10 <td>BG477592</td>	BG477592
19	682.2	22.1	4374	11 <td>AK031307</td>	AK031307
20	681.8	22.0	3921	11 <td>AK084922</td>	AK084922
21	680.2	22.0	4476	11 <td>AK052232</td>	AK052232
22	670.2	21.7	716	10 <td>BF970807</td>	BF970807
23	667	21.6	890	13 <td>B0856543</td>	B0856543
24	664.8	21.5	736	10 <td>BE277845</td>	BE277845
25	660.4	21.4	794	10 <td>AW954605</td>	AW954605
26	656.2	21.2	823	10 <td>BG327694</td>	BG327694
27	645.8	20.9	651	9	AL602452
28	636.6	20.6	643	10 <td>BE408781</td>	BE408781
29	631.8	20.4	685	10 <td>BE265000</td>	BE265000
30	629.8	20.4	703	10 <td>BE384511</td>	BE384511
31	615.2	19.9	926	10 <td>BE326467</td>	BE326467
32	614.4	19.9	746	13 <td>BQ770491</td>	BQ770491
33	614.4	19.9	795	14 <td>CB245479</td>	CB245479
34	612.2	19.8	772	13 <td>B0425051</td>	B0425051
35	611.8	19.8	895	12 <td>B0819955</td>	B0819955
36	608.8	19.7	777	13 <td>B0708655</td>	B0708655
37	604.4	19.5	771	14 <td>CA513024</td>	CA513024
38	589.6	19.1	829	12 <td>B1824613</td>	B1824613
39	589.2	19.0	690	10 <td>BG333712</td>	BG333712
40	588.8	19.0	592	14 <td>CA337090</td>	CA337090
41	588.8	19.0	884	10 <td>BE278944</td>	BE278944
42	578	18.7	603	10 <td>BG334875</td>	BG334875
43	576.8	18.6	852	10 <td>BF306161</td>	BF306161
44	573	18.5	713	10 <td>BE389749</td>	BE389749
45	570.4	18.4	612	10 <td>BG327283</td>	BG327283

ALIGNMENTS

RESULT 1
BC032619
LOCUS
DEFINITION
Homo sapiens, similar to sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A, clone IMAGE:578066, mRNA.
ACCESSION
BC032619
VERSION
BC032619.1 GI:22749800
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens (human)
REFERENCE
1 (bases 1 to 6875)
AUTHORS
Straussberg, R.
TITLE
Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),

Galtersburg, Maryland:
 Web site: <http://www.nisc.nih.gov>
 Contact: nisc_mgenhgti.nih.gov
 Ahlter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Boufield, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Lurie, P., Legaspi, R.,
 Madu, O.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stantipop, S., Thomas, P.J., Touchman, J.W.,
 Turegion, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/ILN at: <http://image.llnl.gov>
 Series: IRK Plate: 69 Row: 0 Column: 4
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 1191659
 This clone has the following problem: retained intron.

FEATURES

Location/Qualifiers

1..6875
 /organism="Homo sapiens"
 /mol_type="mrna"
 /db_xref="taxon:9606"
 /clone="IMAGE:5578066"
 /tissue_type="Skin, melanotic melanoma."
 /clone_lib="NIH_MGC_72"
 /lab_host="DH10B"
 /note="Vector: pCMV-Sport6"

BASE COUNT 1784 a 1795 c 1592 g 1704 t
 ORIGIN

Query Match 99.9%; Score 3089.8; DB 11; Length 6875;
 Best Local Similarity 99.9%; Pred No. 0;
 Matches 3091; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 ATGAGGTCAAGACCTGCTGCTATTTTACACCTGCTACCTTTGCTGGGCTGTTTC
DB 792 ATGAGGTCAAGACCTGCTGCTATTTTACACCTGCTACCTTTGCTGGGCTGTTTC 851
QY 61 CCAGAGATTTGAGGCAATCAAGTATTTGCGATGGCACTATACAAAGATTCGGTGG
DB 852 CCAGAGATTTGAGGCAATCAAGTATTTGCGATGGCACTATACAAAGATTCGGTGG 911
QY 121 TTGTGGGCCCAAGCCAGAGAGCAACACACAGAGGAGGCTGGACATCCAGATG
DB 912 TTGTGGGCCCAAGCCAGAGAGCAACACACAGAGGAGGCTGGACATCCAGATG 971
QY 181 ATTATGATCATGAACGGAACCCCTACATTTGCTGAGGACCATATTTACTGTTGAT
DB 972 ATTATGATCATGAACGGAACCCCTACATTTGCTGAGGACCATATTTACTGTTGAT 1031
QY 241 ATGAGCATCATCAACAGGAAATTTTGTAGCAAAAACCTGACATGAAATCTAGA
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DB 1092 CAGGCGCATGTAGACATGACAGATGAAGGAAAAACATAGAGTAGTGCACAACTTT 1151
QY 361 ATTAAGTCTTCTTAAAGAAAAAGATGATGATTTGCTGTGGAATTAATGCTTTC
DB 1152 ATTAAGTCTTCTTAAAGAAAAAGATGATGATTTGCTGTGGAATTAATGCTTTC 1211
QY 421 AACCGTCTGTCAGAAACATATAGATGATATGATGAACCATTTGGGGATCAATTCAGC
DB 1212 AACCGTCTGTCAGAAACATATAGATGATATGATGAACCATTTGGGGATCAATTCAGC 1271
QY 481 GGAATGGCAGATGCCCATATGATGCCAAACATGGCAAGTGCATGTTTGCAGATGGA
DB 1272 GGAATGGCAGATGCCCATATGATGCCAAACATGGCAAGTGCATGTTTGCAGATGGA 1331
QY 541 AAATTAATCTAGCCACAGTAGTACTTCTTGCATTTGAGCGAGTCAATTAACGGAGT
DB 1332 AAATTAATCTAGCCACAGTAGTACTTCTTGCATTTGAGCGAGTCAATTAACGGAGT 1391

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DB 1392 CTGGAGAAAGCCCTACCTCGGAGCCGTACAGACATTCAAAATGGTGAAGAACA 1451
QY 661 TACTTTGTCAGCCGCTGATTAAGGATTAATATCTTCTTCTTCAAGGAATAGCA 720
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QY 721 GTGAGATTAACACATGGGAAAGGTAGTTTCCCAAGAGTGGCTCAGTTTGAAGAT 780
DB 1512 GTGAGATTAACACATGGGAAAGGTAGTTTCCCAAGAGTGGCTCAGTTTGAAGAT 1571
QY 781 GATATGGAGATCTCAAAAGATCCGAGCAAAACAGTGGACGTCGTCGAGAGCCGCC 840
DB 1572 GATATGGAGATCTCAAAAGATCTGAGCAAAACAGTGGACGTCGTCGAGAGCCGCC 1631
QY 841 TTGACTGCTCACTTCTGAGACCTCATTTTATTTTCAACATTCCTCCAGCAGTTACA 900
DB 1632 TTGACTGCTCACTTCTGAGACCTCATTTTATTTTCAACATTCCTCCAGCAGTTACA 1691
QY 901 GATGATATCTATCAACGGCGCTGATGTTTCTCTGGCAAGTTTCTACACCTTATAC 960
DB 1692 GATGATATCTATCAACGGCGCTGATGTTTCTCTGGCAAGTTTCTACACCTTATAC 1751
QY 961 AGCATCCCTGGGCTGCTGAGTCTGCTATGATGATGATGATGATGATGATGATGAT 1020
DB 1752 AGCATCCCTGGGCTGCTGAGTCTGCTATGATGATGATGATGATGATGATGATGAT 1811
QY 1021 GGGAGATTAAGGAAAGAGATGCTGATATTCACCTGAGACACAGTCTGATGAGCA 1080
DB 1812 GGGAGATTAAGGAAAGAGATGCTGATATTCACCTGAGACACAGTCTGATGAGCA 1871
QY 1081 GTTCCCTAAGCCAGGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1872 GTTCCCTAAGCCAGGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1931
QY 1141 TCCCAATGATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
DB 1932 TCCCAATGATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1991
QY 1201 GGAGTCCCTGCTATCTTCAACAGGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
DB 1992 GGAGTCCCTGCTATCTTCAACAGGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 2051
QY 1261 ACCAAATTTGACAGTGCACAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
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QY 1321 GGATCAGAGAGGGAATCATCTTGAAGTTTGGCCAGAAATAGGAATAGTGGTTTCTA 1380
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QY 1381 AATGACAGCCTTTTCTGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1440
DB 2172 AATGACAGCCTTTTCTGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 2231
QY 1441 GGAGTCAAGACAAAAGATCATGGGATGATGATGATGATGATGATGATGATGATGAT 1500
DB 2232 GGAGTCAAGACAAAAGATCATGGGATGATGATGATGATGATGATGATGATGATGAT 2291
QY 1501 GTTGGTCTCTACCTGTGTGATTAAGGTTCCCTTGGCCGCTGTGAACGATGGGAG 1560
DB 2292 GTTGGTCTCTACCTGTGTGATTAAGGTTCCCTTGGCCGCTGTGAACGATGGGAG 2351
QY 1561 TGTAAAAAACCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
DB 2352 TGTAAAAAACCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2411
QY 1621 GCTGACAGCATTTTATCAACCAAGAGAGATGATGATGATGATGATGATGATGATGAT 1680
DB 2412 GCTGACAGCATTTTATCAACCAAGAGAGATGATGATGATGATGATGATGATGATGAT 2471

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QY 1681 AATACAGATGTCCTGGGGGAGCTGTCAAAATTCCTTTGTGGCACTGAATGGGATTCACAG 1740
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 QY 1861 GGAGTGTCTTCCCATATCACCACAGCAAGAGGAGTATTCGGGAAATTAACCTCAAA 1920
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 QY 2521 ATGGCGCTGAG 2580
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 QY 2641 GTTCCACAGGGGAGGAGGCTCCCGGGTCCCCCGGAGAGCTCCCTGTCTCAGAGCGTCTA 2700
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 QY 2941 GTGACGTCTCTCAG 3000
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RESULT 2
 AK042751
 LOCUS
 DEFINITION
 Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
 enriched library, clone:A730020P05 product:sema domain,
 transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A,
 full insert sequence.

AK042751
 AK042751.1 GI:26335300
 HTG; CAP trapper.
 Mus musculus (house mouse)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE
 1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Kono, H., Akiyama, J., Nishi, K., Kusunagi, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Iwama, M., Ohara, E., Watabiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system—384-format
 sequencing pipeline with 384 multichipillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS
 4
 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishi, Y.,
 Aizawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, T., Fukuda, S.,
 Aizawa, K., Iizawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamada, I.,
 Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
 Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
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Db      1511 CTGACCTGCTGGTGGCTGGAGCTCTCATTTTATTTTCAATATACCTCCAGGAGCTTACA 1570
QY      901  GAGTGAATTCGTAACAAGGGGCTGATGTTGCTGGCAAGTTTCTTACACCTTATAC 960
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Db      2171 GTTGGCTTCTCACTGCTGATGAAGAGTTCCTTGGCGGCTGCTGCTGCTGCTGCTG 2230
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Db      2231 TGTAAAAAACTGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2290
QY      1621 GCTGTGAGCATTATACCCACAGACAGCTGATTTGAGCAGAGCAGATGAGCGTGGC 1680
Db      2291 TCTGTGAGCATTATACCCACAGACAGCTGATTTGAGCAGAGCAGATGAGCGTGGC 2350
QY      1681 AATACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
Db      2351 AATACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2410
QY      1741 TCCCT 1745
Db      2411 CCTCT 2415

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RESULT 3
AK082711 3329 bp mRNA linear HTC 05-DEC-2002
LOCUS AK082711
DEFINITION Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length
enriched library, clone: C230094A19 product: sema domain,
transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A,
full insert sequence.
ACCESSION AK082711
VERSION AK082711.1 GI: 26349884

```

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KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

```

HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253

2
Garninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374

3
Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiyagi, K.,
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Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
RIKEN Integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multichannel sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913

4
Kawai, J., Shingawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
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Wang, K. H., Weitz, C., Whitaker, C., Wilming, L., Wyshaw-Boris, A.,
Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S., and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660

5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
11217851

TITLE
JOURNAL

Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M., and Hayashizaki, Y.
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
Kanagawa 230-0045, Japan (E-mail: genome-resgsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT

CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.

FEATURES

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Location/Qualifiers
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 REFERENCE 1 (bases 1 to 2411)
 AUTHORS Amgen EST Program.
 TITLE Amgen Rat EST Program
 JOURNAL Unpublished
 COMMENT Contact: Dan Fitzpatrick
 Amgen, Inc
 One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
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Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project, 5'-6' end one pass sequencing: Helix
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Helix Research Institute.

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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
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DNA sequencing by: Agencourt Bioscience Corporation (LNL)
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BASE COUNT 235 a 210 c 226 g 219 t 1 others
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Matches 860; Conservative 0; Mismatches 18; Indels 6; Gaps 3;

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Db      728 GACATAGAGCGTGGCAATACAGATGATGGGAGCTGTCACATTTCTTTGGTGGACT 787
QY      1725 GAATGGCATTCACAGTTCCCTCTTGGCCAGACACACACACATGATGAGGCTCAAGA 1784
Db      788 GAATGGCATTCACAGTTCCCTCTTGGCCAGAC-ACCAATACAGATTCACGGCTCAAGA 846
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FEATURES
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High quality sequence stop: 862.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4872704"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NH_MGC_49"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."
BASE COUNT
206 a 300 c 243 g 138 t
ORIGIN
Query Match 25.4%; Score 784.4; DB 12; Length 887;
Best Local Similarity 95.8%; Pred. No. 4e-196;
Matches 849; Conservative 0; Mismatches 31; Indels 6; Gaps 4;
QY 1903 CGGGAAGTTTACCTCAAAAGCCACAGCCAGTGTCCGCTACCCCTTGGCATTTGCA 1962
Db 2 CGGGAAGTTTACCTCAAAAGCCACAGCCAGTGTCCGCTACCCCTTGGCATTTGCA 61
QY 1963 GTGATCTGGGCTTTGCTCATGAGGGGCGCTTTCTCGGCGATCACCGCTTACTGCTGTGT 2022
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QY 2023 GATCATGCGGCGGAAAGAGCTGCTGTGTGTGACGCCAGAGAGAGAGAGTCAACCTCG 2082
Db 122 GATCATGCGGCGGAAAGAGCTGCTGTGTGTGACGCCAGAGAGAGAGAGTCAACCTCG 181
QY 2083 GCGCGGGGCTCCATATAGCAGCGTCACCAAGCTCAGCGGGCTTTGGGGAGCACTCAATCC 2142
Db 182 GCGCGGGGCTCCATATAGCAGCGTCACCAAGCTCAGCGGGCTTTGGGGAGCACTCAATCC 241
QY 2143 AAAGACCCAAAGCCCGAGGCGCATCTCTACGCCCATCATGACAAAGAGAGTCCGCACT 2202
Db 242 AAAGACCCAAAGCCCGAGGCGCATCTCTACGCCCATCATGACAAAGAGAGTCCGCACT 301
QY 2203 CCGGCAACAGCGGCCAAGTGTCTAATAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2262
Db 302 CCGGCAACAGCGGCCAAGTGTCTAATAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 361
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Db 362 CTCCGACCCGAGAGTCAACCCCAAGCTGTGACGAGAAAGCGGAGAGAGAGAGAGAGAG 421
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Db 482 GGCCTCCCTGTGATTTCCACAGGAGCTGCGCCGCGGGGCGTCCCGGAGAGAGAGAGAGAG 541
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 ACCESSION Bg769297
 VERSION Bg769297.1 GI:14079950
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 887)
 NIH-MGC <http://mgc.ncl.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC/DC/DTP
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LMD)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMD at:
<http://image.lnl.gov>

Db	341	TCACCTGACAGCAACAACCCCTTTGGGGGCAATGTCTTCCCATATATCCACAAGACAAGAA	400
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QY	1954	GGCATGCGAGTACCTCTGGCTTTCGTGATGGGGGCGCTCTCTCGGGCATCACCTCTAC	2013
Db	461	GGCATGCGAGTACCTCTGGCTTTCGTGATGGGGGCGCTCTCTCGGGCATCACCTCTAC	520
QY	2014	TGCGTCTGATCATCTGGGCGCAAGAGACGTGGGTGTGGTGCACGCGAAGAGAGAGAGCTC	2073
Db	521	TGCGTCTGATCATCTGGGCGCAAGAGACGTGGGTGTGGTGCACGCGAAGAGAGAGAGCTC	580
QY	2074	ACCCACTGCGCGCGGGGCTCCATGAGCAGCTGCACCAAGCTTACGGGCTCTTGGGGAC	2133
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QY	2134	ACTCATATCCAAAGACCCAAAGCGCGGAGG-CATCTCCAGCGCACTCATGACAGCGCAAG	2193
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QY	2194	CTGCGCACTCCCGGCAACAGCGCCAAAGTGTCTTAAAGAGAGACAGCAGCAGCTGGAC	2253
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QY	2314	CGCGGACACCGCGAGTGGAGAGAGAACCAACCTCATGTGCTCGATGATCAAGAGAGATG	2373
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QY	2434	ATCCCGACCGGTGGTCTCCGCCCATACAGAGAGAGGCTTACACAGCTGATGATGTGAC	2493
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QY	2494	CAGCCCAAAATGAGCGAGGTGGCCAGATGGCTGAGGAGCAGCGCCGCAACTGGAG	2553
Db	1000	--ACCCCAAAATGAGCGAGGTGG--CCAGATGGCGGTGGARBRCCAG--CGSCACACTGGAG	1055
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Db	1056	TWTAGACATCAAGGAATTTAGCAGCAG	1084
RESULT 11			
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LOCUS	ABENOURT_8208159	NIH_MGC_112	Homo sapiens cDNA clone IMAGE:6262572
DEFINITION	5', mRNA sequence.		
ACCESSION	B0678536		
VERSION	B0678536.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	NIH-MGC http://mgc.ncl.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-remail.nih.gov		
	Tissue Procurement: DCTD/DP		
	cDNA Library Preparation: Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Amersham Bioscience Corporation		


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QY      1541 GGTGTAGACACATGAGGAGTGTAAAAAACCGTGTGCTCCACAGACCAATATTG 1600
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QY      1841 ACAGACACAGACCTTTGGGGGAGTGTCTCCATATACCAAGACAGAGAGAGTGA 1900
Db      554 ACAGACACAGACCTTTGGGGGAGTGTCTCCATATACCAAGACAGAGAGAGTGA 613
QY      1901 TTGGGGAAGTTACTCTAAAGGCGACAGACAGTGTGCTCCATACCTCTTGAGCAATG 1960
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QY      1961 CAGTCATCTGAGTGTGATGAGGAGGCGCTCTCTCTGAGGATCATGAGTGTGAGTGTG 2020
Db      674 CAGTCATCTGAGTGTGATGAGGAGGCGCTCTCTCTGAGGATCATGAGTGTGAGTGTG 733
QY      2021 GTGATCATGCGCGCAAGAGAGTGTGAGGAGGCGCAAGAGAGAGAGTGTGAGTGTG 2080
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QY      2081 CGGCGCGGGG 2090
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 B0440312
 VERSION
 B0440312.1 GI:21179388
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS
 NIH-MGC http://mgc.nci.nih.gov/
 1 (bases 1 to 864)
 TITLE
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 CONTACT
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rtmail.nih.gov
 Tissue Procurement: ATCC/DCMP/DTF
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.lnl.gov>
 Plate: L14M13504 row: c column: 07
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 Average insert size 2 kb. Library constructed by Life
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 204 a 273 c 232 g 150 t 5 others

Query Match
 Best Local Similarity 96.3%; Pred. No. 2.5e-192;
 Matches 830; Conservative 0; Mismatches 24; Indels 8; Gaps 4;

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QY      1896 AGTGAATTCGGGAAAGTTACTCTAAAGGCGACAGACAGTGTGCTCCATACCTCTTGAGC 1955
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QY      2256 GACGGCGCTCCCGCACCGAGTGTCAACCCAGCGTGTGAGAGAGGAGAGAGAGAGAGAG 2315
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QY	2374	CCCCCATATGGG--CTCCCTCTGTATTCCACGAGACCTG----	2427
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Db	841	AGCACATATCCCGACGAGGGG 862	
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DEFINITION B0838082 5' mRNA sequence.			
ACCESSION B0838082.1 GI:24022477			
VERSION B0838082.1 GI:24022477			
KEYWORDS EST.			
SOURCE Homo sapiens (human)			
ORGANISM Homo sapiens			
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.			
TITLE NIH-MGC http://mgi.nci.nih.gov/.			
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)			
COMMENT Unpublished			
Contact: Robert Strausberg, Ph.D.			
Email: gcapds@email.nih.gov			
Tissue Procurement: DCPD/DTF			
cDNA Library Preparation: Rubin Laboratory			
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
Clone distribution: MGC Clone Distribution Information can be			
found through the I.M.A.G.E. Consortium/LLNL at:			
http://image.llnl.gov			
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EcoRI; cDNA made by oligo-dT priming. Directionally cloned			
into EcoRI/XhoI sites using the following 5' adaptor:			
GGCAGAG(G). Library constructed by Ling Hong in the			
laboratory of Gerald M. Rubin (University of California,			
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and			
Superscript II RT (Life Technologies). Note: This is a			
NIH_MGC Library."			
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QY	1526	AGSTTCCCTTGGCCGCTGTGAACGACATGGGAAGTGTAAAAAAACCCTGTATGGCTTCCA	1585		
Dd	241	AGGTTCCCTTGGCCGCTGTGAACGACATGGGAAGTGTAAAAAAACCCTGTATGGCTTCCA	300		
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Dd	301	GAGACCCATATTGTGTGATGATTAAGAAAGGTGTGTGCTGCCACCACTTTATTCACCAACA	360		
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Dd	601	ACAAGAAGGAGTATTCGGGAAAGTTACCTCAAAGGCGCACAGCAGCTGTCCCTGCA	660		
QY	1946	CCCTCTTGGCCATTCAGATCATCTCGGCTTTCGTCATGGGGGCGCTTCTTGGGSCATCA	2005		
Dd	661	CCCTCTTGGCCATTCAGATCATCTCGGCTTTCGTCATGGGGGCGCTTCTTGGGSCATCA	720		
QY	2006	CCGCTTACTCGCTCTGTGATCATTCGGCGCAAAAGACGTGGCTGTGGTGCAGCGCAAG	2062		
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DEFINITION	AGENCOURT_B208014 NIH_MGC_112 Homo sapiens cdna clone IMAGE:6282587				
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VERSION	B0683009.1				
KEYWORDS	EST.				
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ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/				
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)				
TITLE	Unpublished				
JOURNAL	Contact: Robert Strausberg, Ph.D.				
COMMENT	Email: cga@phs-remai.nih.gov Tissue Procurement: DCTD/DTP CDNA Library Preparation: Rubin Laboratory DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL) Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LHCW2425 row: c column: 04 High quality sequence stop: 621. Location/Qualifiers:				

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/notes="Organ: skin; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dt priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using Zap-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC library."
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BASE COUNT 221 a 220 c 245 g 204 t

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Query Match 24.6%; Score 760.6; DB 13; Length 890;
Best Local Similarity 97.0%; Pred. No. 8e-190;
Matches 808; Conservative 0; Mismatches 19; Indels 6; Gaps 3;

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QY 1406 TGAGTGTTAACACTGTGAAAAATGACCTATGATGATGATGATGATGATGATGATGATG 1465
DB 121 TGAGTGTTAACACTGTGAAAAATGACCTATGATGATGATGATGATGATGATGATGATG 180
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DB 181 GCATGCACTGCAAGAGACAGCAAGCACTCTGTATGTTGCGTTCTCTACTGTTGATAA 240
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 30, 2003, 16:34:33 ; Search time 11072.7 Seconds
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Title: US-09-856-681-1

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Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
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Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

Score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	3093	100.0	3862	9	AX026746 Sequence
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7	2746.2	88.8	3550	6	AX099520 Homo sapi
8	2414.8	78.1	3018	10	AF288666 Mus muscu
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ACCESSION AX026741
VERSION AX026741.1 GI:10187886
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Klostermann, A. and Behl, C.
TITLE Human semaphorin 6a-1 (sema6a-1), a gene involved in neuronal development and regeneration mechanisms during apoptosis, and its

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RESULT 2

AX026746

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 Klostermann, A. and Behl, C.

Human semaphorin 6a-1 (sema6a-1), a gene involved in neuronal development and regeneration mechanisms during apoptosis, and its use as a potential drug target

Patent: WO 0031252-A 6 02-JUN-2000.

KLOSTERMANN ANDREAS (DE) ; MAX PLANCK GESAMTSCHAFT (DE) ; BEHL CHRISTIAN (DE)

FEATURES

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ORIGIN

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QY	961	AGCATCCCTGGGCTGTCAGTCTGTGCTCTATGACATGTTTACATTTGCCAGTGTGTTTACT	1020
Db	1618	AGCATCCCTGGGCTGTCAGTCTGTGCTCTATGACATGTTTACATTTGCCAGTGTGTTTACT	1677
QY	1021	GGGAGATTCAAGAAACAGAGTCTCTCGATTTCCACCGTGGACACAGAGTCTCGATGAAACGA	1080
Db	1678	GGGAGATTCAAGAAACAGAGTCTCTCGATTTCCACCGTGGACACAGAGTCTCGATGAAACGA	1737
QY	1081	GTTCCTTAAGCCCAAGGCAAGTGTGCTGTGCTGCTCATCTCTTAAGAAAGATATGCAAC	1140
Db	1738	GTTCCTTAAGCCCAAGGCAAGTGTGCTGTGCTGCTCATCTCTTAAGAAAGATATGCAAC	1797
QY	1141	TCCAATAGTTCCTGATGATACCTCGAATTTATCAAGAAGCAACCCGCTCATGATGTAG	1200
Db	1798	TCCAATAGTTCCTGATGATACCTCGAATTTATCAAGAAGCAACCCGCTCATGATGTAG	1857

QY	1201	GCAGTGGCCCTCATCTTCAACAGCGCCATGTCCTCTGAGAACAAATGTCAGATACCGCCTT	1260
Db	1858	GCAGTGGCCCTCATCTTCAACAGCGCCATGTCCTCTGAGAACAAATGTCAGATACCGCCTT	1917
QY	1261	ACCAAAATTCGAGTGGACACAGCTGCTGGGCCATATCAGAAATCACACTGGTGGTTTTCTG	1320
Db	1918	ACCAAAATTCGAGTGGACACAGCTGCTGGGCCATATCAGAAATCACACTGGTGGTTTTCTG	1977
QY	1331	GGATCAGAAAGGGAATCATCTTGAAGTTTTTGGCCAGATAAGGAATATAGTGGTTTTCTA	1380
Db	1978	GGATCAGAAAGGGAATCATCTTGAAGTTTTTGGCCAGATAAGGAATATAGTGGTTTTCTA	2037
QY	1381	AATGACACCTTTTCTCTGGAGAGATGAGTGTTTTACACTCTGAAAATATGACATATGAT	1440
Db	2038	AATGACACCTTTTCTCTGGAGAGATGAGTGTTTTACACTCTGAAAATATGACATATGAT	2097
QY	1441	GGAGTCGAAGCAAAAGAGATCAVGGGCATGTCAGCTGGACAGACAGCAAGCAGCTCTGTAT	1500
Db	2098	GGAGTCGAAGCAAAAGAGATCAVGGGCATGTCAGCTGGACAGACAGCAAGCAGCTCTGTAT	2157
QY	1501	GTTGCGTCTTACCCTGTGTATAAAGTTCCCTTGGCCGCGTGTGAACGACATGGGAAG	1560
Db	2158	GTTGCGTCTTACCCTGTGTATAAAGTTCCCTTGGCCGCGTGTGAACGACATGGGAAG	2217
QY	1561	TGTAAAAAAACCTGTATATGCTCCAGAACCATTTTGGATGGATAAAGGAAGTGGT	1620
Db	2218	TGTAAAAAAACCTGTATATGCTCCAGAACCATTTTGGATGGATAAAGGAAGTGGT	2277
QY	1621	GCCTCGACCCATTATATACCCACAGACGAGCTGACTTTTGGACAGACATATAGCGTGGC	1680
Db	2278	GCCTCGACCCATTATATACCCACAGACGAGCTGACTTTTGGACAGACATATAGCGTGGC	2337
QY	1681	AATACACATGSGTCTGGGGGAGCTGTGCACATTCCTTTGGGACATGAAAGGGCATTCAGT	1740
Db	2338	AATACACATGSGTCTGGGGGAGCTGTGCACATTCCTTTGGGACATGAAAGGGCATTCAGT	2397
QY	1741	TCCCTCTTGGCCACAGCACACCATCTCAGATTGCAAGGCTCAAGAGGGGTATGAGTCTAGG	1800
Db	2398	TCCCTCTTGGCCACAGCACACCATCTCAGATTGCAAGGCTCAAGAGGGGTATGAGTCTAGG	2457
QY	1801	GGAGGAATGCTGGACATGGAAGCATCTCTTGACTGACTGACAGCACAGACCCCTTTGGGG	1860
Db	2458	GGAGGAATGCTGGACATGGAAGCATCTCTTGACTGACTGACAGCACAGACCCCTTTGGGG	2517
QY	1861	GCAGTGTCTTCCCATATATCACCAAGACAAAGAGAGAGTGATTCGGGAAAGTTACTCTCAA	1920
Db	2518	GCAGTGTCTTCCCATATATCACCAAGACAAAGAGAGAGTGATTCGGGAAAGTTACTCTCAA	2577
QY	1921	GGCACAAGACAGCTGTTCCCGTACCCTCTTGGCCATTGCAGTCAATCTGGCTTGGTC	1980
Db	2578	GGCACAAGACAGCTGTTCCCGTACCCTCTTGGCCATTGCAGTCAATCTGGCTTGGTC	2637
QY	1981	ATGGGGGGCGTCTTCTCGGGCATCACCGTACTCGTGCTGTATCTCATTCGGCGCAAGAGAC	2040
Db	2638	ATGGGGGGCGTCTTCTCGGGCATCACCGTACTCGTGCTGTATCTCATTCGGCGCAAGAGAC	2697
QY	2041	GTTGGCTGTGTGACGCGCAAGAGAGAGAGACTCACCCATCTCGCGCGGGCTCCATAGAC	2100
Db	2698	GTTGGCTGTGTGACGCGCGCAAGAGAGAGAGACTCACCCATCTCGCGCGGGCTCCATAGAC	2757
QY	2101	AGCGTACAGCAAGTCAAGCGGCGCTTTTGGGGAACATCAATCCAAAGACCCAAAGCCGGAG	2160
Db	2758	AGCGTACAGCAAGTCAAGCGGCGCTTTTGGGGAACATCAATCCAAAGACCCAAAGCCGGAG	2817
QY	2161	GGCATCTCTACGCCCATCTGACAAACAGCGCAAGCTCGCCACTCCGGCAACAGGCCCAAG	2220
Db	2818	GGCATCTCTACGCCCATCTGACAAACAGCGCAAGCTCGCCACTCCGGCAACAGGCCCAAG	2877
QY	2221	ATGTCATTAAGAAGCAAGACAGACACCACTGAGACTAGAGGCGCTCCCCACCCAGAGTCA	2280
Db	2878	ATGTCATTAAGAAGCAAGACAGACACCACTGAGACTAGAGGCGCTCCCCACCCAGAGTCA	2937

OY 301 CAGGCCGATGTAGACATGTGCAATGAAGGAAACATTAAGATAGTCCCACTT 360
 |||||
 Db 550 CAGGCCGATGTAGACATGTGCAATGAAGGAAACATTAAGATAGTCCCACTT 609
 OY 361 ATTAAGTCTCTTAAGAAAAAGATGATGATGTTTGTCTGTGAACATATGCTTC 420
 |||||
 Db 610 ATTAAGTCTCTTAAGAAAAAGATGATGATGTTTGTCTGTGAACATATGCTTC 669
 OY 421 AACCTTCTCGAGAACTATTAAGATGATGATGTTTGTCTGTGAACATATGCTTC 480
 |||||
 Db 670 AACCTTCTCGAGAACTATTAAGATGATGATGTTTGTCTGTGAACATATGCTTC 729
 OY 481 GGATGCGCAGATGCGCCATATGATGCAAAACATGCAACGTTGCTGCTGATGCA 540
 |||||
 Db 730 GGATGCGCAGATGCGCCATATGATGCAAAACATGCAACGTTGCTGCTGATGCA 789
 OY 541 AACCTATCTAGCAGCAGTACTGATGCTTCTGCTGCTGCTGCTGCTGCTGCTG 600
 |||||
 Db 790 AACCTATCTAGCAGCAGTACTGATGCTTCTGCTGCTGCTGCTGCTGCTGCTG 849
 OY 601 CTGAGAAAGCCCTACCTGCGGACCGTCAAGCAGTCAAAATGTTGAAGAACCA 660
 |||||
 Db 850 CTGAGAAAGCCCTACCTGCGGACCGTCAAGCAGTCAAAATGTTGAAGAACCA 909
 OY 661 TACTTGTTCAGCCGCGATTAAGGATTAATCTACTTCTTCTGAGGAAATGCA 720
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 Db 910 TACTTGTTCAGCCGCGATTAAGGATTAATCTACTTCTTCTGAGGAAATGCA 969
 OY 721 GTGAGTAAACACCATGGAAGAGTACTTCCCAAGTGGCTCAGTGTGAAGAT 780
 |||||
 Db 970 GTGAGTAAACACCATGGAAGAGTACTTCCCAAGTGGCTCAGTGTGAAGAT 1029
 OY 781 GATATGGAAGATCTCAAGAGTCTCTGAGAAACAGTGGCTCAGTGTGAAGAT 840
 |||||
 Db 1030 GATATGGAAGATCTCAAGAGTCTCTGAGAAACAGTGGCTCAGTGTGAAGAT 1089
 OY 841 TTGAAGTCTCAAGTCTCTGAGAAACAGTGGCTCAGTGTGAAGAT 900
 |||||
 Db 1090 TTGAAGTCTCAAGTCTCTGAGAAACAGTGGCTCAGTGTGAAGAT 1149
 OY 901 GATGATGTATCAACAGGCGCTGATGTTGCTGCAACGTTTCTACACCTTAAAC 960
 |||||
 Db 1150 GATGATGTATCAACAGGCGCTGATGTTGCTGCAACGTTTCTACACCTTAAAC 1209
 OY 961 AGCATGCGGCTGATGATGCTGCTATGATGATGATGATGATGATGATGATG 1020
 |||||
 Db 1210 AGCATGCGGCTGATGATGCTGCTATGATGATGATGATGATGATGATGATG 1269
 OY 1021 GGGAGATTCAGAGAAAGTCTCTGATTCACCTGAGACACAGTCTGATGACGA 1080
 |||||
 Db 1270 GGGAGATTCAGAGAAAGTCTCTGATTCACCTGAGACACAGTCTGATGACGA 1139
 OY 1081 GTTCTTAAGCCGAGGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
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 Db 1330 GTTCTTAAGCCGAGGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1189
 OY 1141 TCCATGAGTCTCCGATGATACCTGAATTCATCAAGACGACCCCTCATGATGAG 1200
 |||||
 Db 1390 TCCATGAGTCTCCGATGATACCTGAATTCATCAAGACGACCCCTCATGATGAG 1449
 OY 1201 GCGATGCGCTCCATCTTCAACGCGCATGTTCTGAGAACAAATGCTGATGCGCT 1260
 |||||
 Db 1450 GCGATGCGCTCCATCTTCAACGCGCATGTTCTGAGAACAAATGCTGATGCGCT 1509
 OY 1261 ACCAAATGCGAGTGCACAGCTGCTGCGCATATCAGATCAGACTGCTGTTTCTG 1320
 |||||
 Db 1510 ACCAAATGCGAGTGCACAGCTGCTGCGCATATCAGATCAGACTGCTGTTTCTG 1569
 OY 1321 GGAATGAGAGGGAATCTGAGATTTTGGCGAGATGAGAAATAGTGTCTTCA 1380
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 Db 1570 GGAATGAGAGGGAATCTGAGATTTTGGCGAGATGAGAAATAGTGTCTTCA 1629

OY 1381 AATGACAGCCTTTCTCTGAGAGATGATGTTTACACTCTGAAATAATGACATATGAT 1440
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 Db 1630 AATGACAGCCTTTCTCTGAGAGATGATGTTTACACTCTGAAATAATGACATATGAT 1689
 OY 1441 GGAATGAGAGGGAATCTGAGATTTTGGCGAGATGAGAAATAGTGTCTTCA 1500
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 Db 1690 GGAATGAGAGGGAATCTGAGATTTTGGCGAGATGAGAAATAGTGTCTTCA 1749
 OY 1501 GTTGTGCTCTACCTGCTGATTAAGGTTCCCTTGGCGGCTGTAAGGATGGAAG 1560
 |||||
 Db 1750 GTTGTGCTCTACCTGCTGATTAAGGTTCCCTTGGCGGCTGTAAGGATGGAAG 1809
 OY 1561 TGTAAAAAACCCTGATGTTGCTTCCAGAGACCCATATGATGATTAAGAGTGTGT 1620
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 Db 1810 TGTAAAAAACCCTGATGTTGCTTCCAGAGACCCATATGATGATTAAGAGTGTGT 1869
 OY 1621 GCTGAGCCTTATATACCAACAGCAGACTGATCTTTGAGCAGGATATGAGCCTGGC 1680
 |||||
 Db 1870 GCTGAGCCTTATATACCAACAGCAGACTGATCTTTGAGCAGGATATGAGCCTGGC 1929
 OY 1681 AATGACAGTGTGAGGAGCTGACATATCTTGTGGCAGTGA----- 1726
 |||||
 Db 1930 AATGACAGTGTGAGGAGCTGACATATCTTGTGGCAGTGA----- 1989
 OY 1727 -----ATGGCAGTCCAGTTCCTCTG 1749
 |||||
 Db 1990 CCTTACAGATTAATGAAATGCTTACCAACAGATGATGAGGATTCAGTTCCTCTG 2049
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 OY 1750 CCGACAGACCCATCAGATTCAGGCTCAGAGGAGGATTAAGTCTGAGGAGAAATG 1809
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 Db 2050 CCGACAGACCCATCAGATTCAGGCTCAGAGGAGGATTAAGTCTGAGGAGAAATG 2109
 OY 1810 CTGAGCTGAGACATCTGTTGATCTGATGATGATGATGATGATGATGATGATG 1869
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 Db 2110 CTGAGCTGAGACATCTGTTGATCTGATGATGATGATGATGATGATGATGATG 2169
 OY 1870 TCCCATTAATCAGCAAGAGAGAGGATGATGATGATGATGATGATGATGATGATG 1929
 |||||
 Db 2170 TCCCATTAATCAGCAAGAGAGAGGATGATGATGATGATGATGATGATGATGATG 2229
 OY 1930 CAGCTGTTCCCTCTCAGCCTTGTGCGATTTGATGATGATGATGATGATGATGATG 2289
 |||||
 Db 2230 CAGCTGTTCCCTCTCAGCCTTGTGCGATTTGATGATGATGATGATGATGATGATG 2349
 OY 1990 GTTCTGCGGATCAACGCTGATGATGATGATGATGATGATGATGATGATGATG 2049
 |||||
 Db 2290 GTTCTGCGGATCAACGCTGATGATGATGATGATGATGATGATGATGATGATG 2349
 OY 2050 GTGACAGCAGAGAGAGAGAGTCAACCTGCGGCGGAGCTCATGAGAGAGCTCAC 2109
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 Db 2350 GTGACAGCAGAGAGAGAGAGTCAACCTGCGGCGGAGCTCATGAGAGAGCTCAC 2409
 OY 2110 AAGCTCAAGCGGCTCTTGGGAGCAGTCAATCCAAAGAGAGAGAGAGAGAGAGAG 2169
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 Db 2410 AAGCTCAAGCGGCTCTTGGGAGCAGTCAATCCAAAGAGAGAGAGAGAGAGAGAG 2469
 OY 2170 ACGCAGTCAATGACAGAGAGAGAGTCCGACCTGCGGAGAGAGAGAGAGAGAGAG 2229
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 Db 2470 ACGCAGTCAATGACAGAGAGAGAGTCCGACCTGCGGAGAGAGAGAGAGAGAGAG 2529
 OY 2230 AAAGCAGACAGCAGCAGCAGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2289
 |||||
 Db 2530 AAAGCAGACAGCAGCAGCAGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2589
 OY 2290 CTGACAG 2349
 |||||
 Db 2590 CTGACAG 2649
 OY 2350 ATCAATGCTGAGCAAG 2409
 |||||
 Db 2650 ATCAATGCTGAGCAAG 2709
 OY 2410 CCGCTGCGGAG 2469

D	b	781	TTTTCACATTTCTCCAGCAGTTACAGATGTGATTCCTATCAACAAGGGCCGATAGTTGTCTC	840
Q	y	936	GGCAACGTTTCTTACACCTTATPACAGCATCCCTGGGTCTGCAGTGTGCTATGACAT	995
D	b	841	GGCAACGTTTCTTACACCTTATPACAGCATCCCTGGGTCTGCAGTGTGCTATGACAT	900
Q	y	996	GCCTGCATGTCCGACGTTTCTTCTGTGGAGATTCAAGGAAACAAGAACTCCGATTCCAC	1055
D	b	901	GCCTGCATGTCCGACGTTTCTTCTGTGGAGATTCAAGGAAACAAGAACTCCGATTCCAC	960
Q	y	1056	CTGGACACCAAGTTCCTGATGAACGATTCCTAAGCCACGACAGGTGTGCTGTGGCTC	1115
D	b	961	CTGGACACCAAGTTCCTGATGAACGATTCCTAAGCCACGACAGGTGTGCTGTGGCTC	1020
Q	y	1116	ATCCTCCTTGAAGAAAGTATGCCAACCCGAAATGATGCTCCCTGATGATACCTGAACCTCAT	1175
D	b	1021	ATCCTCCTTGAAGAAAGTATGCCAACCCGAAATGATGCTCCCTGATGATACCTGAACCTCAT	1080
Q	y	1176	CAAGACGACACCCCTCATGATGATGAGCAGTGGCCCTCATCTTCCACAGGACGATGTCTCT	1235
D	b	1081	CAAGACGACACCCCTCATGATGATGAGGAGTGGCCCTCATCTTCCACAGGACGATGTCTCT	1140
Q	y	1236	GACAAACATGTGATGATACCGCTTTACCAAAATTGCAGTGGACACAGCTGTCTGGCCATA	1295
D	b	1141	GAGAAACATGTGATGATACCGCTTTACCAAAATTGCAGTGGACACAGCTGTCTGGCCATA	1200
Q	y	1296	TCAGAAATCACACGTGGTTTCTTGTGGATTCGAGAGGAGGAAATCATCTTGAAGTTTGGC	1355
D	b	1201	TCAGAAATCACACGTGGTTTCTTGTGGATTCAGAGAGGAGGAAATCATCTTGAAGTTTGGC	1260
Q	y	1356	CAGAAATGAAATATGTGTTTCTTAAATGACAGCCTTTTCTGGAGACATGATGCTTTTA	1415
D	b	1261	CAGAAATGAAATATGTGTTTCTTAAATGACAGCCTTTTCTGGAGACATGATGCTTTTA	1320
Q	y	1416	CAACTCTG-AAAAATGACGATGATGATGATGCGAAGCAAAAGGATCATGGGATGACG	1474
D	b	1321	CAACTCTGAAAAATGACGATGATGATGATGCGAAGCAAAAGGATCATGGGATGACG	1380
Q	y	1475	TGGACAGACGACAGCAGCTCTGTATGTTCGGTTCCTTACCTGTGTATAAAGTTTCCC	1534
D	b	1381	TGGACAGACGACAGCAGCTCTGTATGTTCGGTTCCTTACCTGTGTATAAAGTTTCCC	1440
Q	y	1535	TTGGCCGGGTGGAACGACATGGGGAAGGT-AAAAAAACGTAAATGGCTCCACAGACCCA	1593
D	b	1441	TTGGCCGGGTGGAACGACATGGGGAAGGTAAAAAAACGTAAATGGCTCCACAGACCCA	1500
Q	y	1594	TATGTGGATGATAAAGAAAGAGTGGTGGCTGCAGCAATTATATCCCAACAGCAGACTG	1653
D	b	1501	TATGTGGATGATAAAGAAAGAGTGGTGGCTGCAGCAATTATATCCCAACAGCAGACTG	1560
Q	y	1654	ACTTTTGGACGACATAGAGCGTGGCAATACAGATGCTCTGGGGGACTGTCACAATTCC	1713
D	b	1561	ACTTTTGGACGACATAGAGCGTGGCAATACAGATGCTCTGGGGGACTGTCACAAAATCC	1620
Q	y	1714	TTTGGGAGCATGAATGGGCAATTCAGTTCCTCTGGCCACACACACATCAGATCTCG	1773
D	b	1621	TTTGGGAGCATGAATGGGCAATTCAGTTCCTCTGGCCACACACACATCAGATCTCG	1680
Q	y	1774	ACGGCTCAAGAGGGGTATGAGTCTAAGGGGAAGAACTCTGACTGGAACATCTGCTTGAC	1833
D	b	1681	ACGGCTCAAGAGGGGTATGAGTCTAAGGGGAAGAACTCTGACTGGAACATCTGCTTGAC	1740
Q	y	1834	TCACCTGACACACAGACCCCTTTGGGGGCACTGTCTTCCATATCACCAAGACAAAGAG	1893
D	b	1741	TCACCTGACACACAGACCCCTTTGGGGGCACTGTCTTCCATATCACCAAGACAAAGAG	1800
Q	y	1894	GGAGTGAATTCGGGAAAGTTTACCTCAAAAGCCACGACACAGCTGTGTCCGTCAACCTCTTG	1953
D	b	1801	GGAGTGAATTCGGGAAAGTTTACCTCAAAAGCCACGACACAGCTGTGTCCGTCAACCTCTTG	1860
Q	y	1954	GCCATTTGACATCCTCTGGCTTGTGTGATGATGGGGGCGCTTCTCTGGGGATCAACGCTTAC	2013
D	b	1861	GCCATTTGACATCCTCTGGCTTGTGTGATGATGGGGGCGCTTCTCTGGGGATCAACGCTTAC	1920

QY	2014	TGCGTGTGTATCATCGGCGCCAAAGACGTCGCTGTGTCGACGCGCAAGGAGAAAGGAGCGTC	2073
Db	1921	TGCGTGTGTATCATCGGCGCCAAAGACGTCGCTGTGTCGACGCGCAAGGAGAAAGGAGCGTC	1980
QY	2074	ACCACACGCGCGCGGGCTCCATGAGACAGGTCACCAAGCTCAGAGCGGCTCTTTGGGAC	2133
Db	1981	ACCACACGCGCGCGGGCTCCATGAGACAGGTCACCAAGCTCAGAGCGGCTCTTTGGGAC	2040
QY	2134	ACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTACGCGCATCTGACACAAACGGCAAG	2193
Db	2041	ACTCAATCCGAAGACCCAAAGCCGGAGGCCATCCTACGCGCATCTGACACAAACGGCAAG	2100
QY	2194	CTGCGCACTCCCGGCAACACGGCGCAAGATCTCATTTAAACACACAGCACACCACTGGAC	2253
Db	2101	CTGCGCACTCCCGGCAACACGGCGCAAGATCTCATTTAAACACACAGCACACCACTGGAC	2160
QY	2254	CTGACGGGCTCCGCCACCCAGAGTCAACCCCAACGGCTGACGACGAGAGCGGAAAGCCACG	2313
Db	2161	CTGACGGGCTCCGCCACCCAGAGTCAACCCCAACGGCTGACGACGAGAGCGGAAAGCCACG	2220
QY	2314	CGCGGACGCCCGAGTGGGAGAGGAAACCAACCTCATCATGCGCTGACACAAAGGACATG	2373
Db	2221	CGCGGACGCCCGAGTGGGAGAGGAAACCAACCTCATCATGCGCTGACACAAAGGACATG	2280
QY	2374	CCCCCATAGGGCTCCCCGTGTGATTCGCCACGAGACTGCCCCCTGGCGGCTCCGCCAGCCAC	2433
Db	2281	CCCCCATAGGGCTCCCCGTGTGATTCGCCACGAGACTGCCCCCTGGCGGCTCCGCCAGCCAC	2340
QY	2434	ATCCCCAGCGGTGTGTCTCTCCCATCAGCAGAGGGGCTACACAGCATGATGATGCTGGAC	2493
Db	2341	ATCCCCAGCGGTGTGTCTCTCCCATCAGCAGAGGGGCTACACAGCATGATGATGCTGGAC	2400
QY	2494	CAGCCCAAAATGAGAGGAGGTGGCCAGATGCGCTGGAGAGACAGGCGCCGACACCTGGAG	2553
Db	2401	CAGCCCAAAATGAGAGGAGGTGGCCAGATGCGCTGGAGAGACAGGCGCCGACACCTGGAG	2460
QY	2554	TATAAGACCATCAAGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTG	2613
Db	2461	TATAAGACCATCAAGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTG	2520
QY	2614	GAGAACCTGGACAGCGCTGCCCCCAAAATTCACAGGAGGGAGGCGCTCCCTGGGTCGCCCG	2673
Db	2521	GAGAACCTGGACAGCGCTGCCCCCAAAATTCACAGGAGGGAGGCGCTCCCTGGGTCGCCCG	2580
QY	2674	GGAGCGTCCCTGTCTCAGACCGGTCCTAAGCAAGCGGGCTGGAATATGCACCACTCCTTTC	2733
Db	2581	GGAGCGTCCCTGTCTCAGACCGGTCCTAAGCAAGCGGGCTGGAATATGCACCACTCCTTTC	2640
QY	2734	TACGGGGTTGACTATTAAGAGAGCTACCCCCAGAACTCGGTCACAGAAAGCACACAGGC	2793
Db	2641	TACGGGGTTGACTATTAAGAGAGCTACCCCCAGAACTCGGTCACAGAAAGCACACAGGC	2700
QY	2794	ACCACCTCAAAAGAAAGACACTAATCTCTCCATTCCTCTCACTCTCCAGAAACAG	2853
Db	2701	ACCACCTCAAAAGAAAGACACTAATCTCTCCATTCCTCTCACTCTCCAGAAACAG	2760
QY	2854	AGCTTTGGCAGGGAGACACCCGCGCGCCCGCCGACAGAGGGTGGACTCCATCCAAAGTG	2913
Db	2761	AGCTTTGGCAGGGAGAGACACCCGCGCGCCCGCCGACAGAGGGTGGACTCCATCCAAAGTG	2820
QY	2914	CACAGCTCCAGCATCTGGCAGGCGGTGACTGTCTGAGAGCAAGCCAGCTCAAGGCC	2973
Db	2821	CACAGCTCCAGCATCTGGCAGGCGGTGACTGTCTGAGAGCAAGCCAGCTCAAGGCC	2880
QY	2974	TACAACTCACTGACAAAGTCGGGGGTGAAGCGGTACGCCCTGCTTAAAGCCGGACGTACCC	3033
Db	2881	TACAACTCACTGACAAAGTCGGGGGTGAAGCGGTACGCCCTGCTTAAAGCCGGACGTACCC	2940
QY	3034	CCCAAAACATCTCTTGTCTCCCTTCCACATCCATGAGAGCCCAATGATGCTGTACATAA	3093
Db	2941	CCCAAAACATCTCTTGTCTCCCTTCCACATCCATGAGAGCCCAATGATGCTGTACATAA	3000

RESULT 6
 AK027867
 LOCUS
 DEFINITION Homo sapiens cDNA FLJ14961 fis, clone PLACE4000230, highly similar
 to Mus musculus semaphorin 1A mRNA.
 AK027867 6060 bp mRNA linear PRI 01-AUG-2002
 AK027867.1 GI:14042853
 VERSION oligo capping; fis (full insert sequence).
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 TITLE
 AUTHORS
 JOURNAL
 COMMENT
 FEATURES
 SOURCE
 CDS
 BASE COUNT
 ORIGIN
 Query Match 96.0%; Score 2969.6; DB 9; Length 6060;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2994; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

Db 121 TAGGACCATATTATTAAGTGTGATATAGACACATCACACAGGAAGAAATTTATTAG 180
 QY 276 CAAAAACTGACATGGAATCTAGACAGCCGATGTACACACATCGACAAATGGAAGAA 335
 Db 181 CAAAAACTGACATGGAATCTAGACAGCCGATGTACACACATCGACAAATGGAAGAA 240
 QY 336 ACATAGAGATAGTGTCCACCACTTATTAAGTTCTTAAAGAAAGCATGATGCTT 395
 Db 241 ACATAGAGATAGTGTCCACCACTTATTAAGTTCTTAAAGAAAGCATGATGCTT 300
 QY 396 GTTGTCTGTGAATTAATGCTTCAACCTCTCTGAGAAATTAAGATGATACAT 455
 Db 301 GTTGTCTGTGAATTAATGCTTCAACCTCTCTGAGAAATTAAGATGATACAT 360
 QY 456 GGAAACATGCGGGATGATTTAGCGGAATGCGGATGCGGATGCGGATGCGGATGCG 515
 Db 361 GGAAACATGCGGGATGATTTAGCGGAATGCGGATGCGGATGCGGATGCGGATGCG 420
 QY 516 CAAGTTGACATGTTGACATGATGGAATACTATACAGCCACAGTACGATGCTTCTG 575
 Db 421 CAAGTTGACATGTTGACATGATGGAATACTATACAGCCACAGTACGATGCTTCTG 480
 QY 576 CATGACGACATGTTTACCGGATGTTGAGAAAGCCCTACCTGCGGACCGTCAAGCA 635
 Db 481 CATGACGACATGTTTACCGGATGTTGAGAAAGCCCTACCTGCGGACCGTCAAGCA 540
 QY 636 CGATTCATAATGTTGAAAGAAACATCTTCTTCAAGCCGATGATGAGATATAT 695
 Db 541 CGATTCATAATGTTGAAAGAAACATCTTCTTCAAGCCGATGATGAGATATAT 600
 QY 696 CTACTTCTCTCAGGAAATGACATGATGATTAACACATGGAAGATGATTTTCC 755
 Db 601 CTACTTCTCTCAGGAAATGACATGATGATTAACACATGGAAGATGATTTTCC 660
 QY 756 AAGAGTGTGCTAGTTTGAAGATGATGAGAGATCTCAAGAGTCTGTGAGAAACA 815
 Db 661 AAGAGTGTGCTAGTTTGAAGATGATGAGAGATCTCAAGAGTCTGTGAGAAACA 720
 QY 816 GTGAGCTGTCTCTAAGCGCGCTGAAGCTGCTGAGTCTGAGATCTCATTTT 875
 Db 721 GTGAGCTGTCTCTAAGCGCGCTGAAGCTGCTGAGTCTGAGATCTCATTTT 780
 QY 876 TTTGACATTTCTCAGGAGTACAGATGATGATTAACAGGCGGTGATGCTTCT 935
 Db 781 TTTGACATTTCTCAGGAGTACAGATGATGATTAACAGGCGGTGATGCTTCT 840
 QY 936 GGCACAGTTTCTACACCTTATTAACAGATCTCTGAGTCTGTGCTATGACAT 995
 Db 841 GGCACAGTTTCTACACCTTATTAACAGATCTCTGAGTCTGTGCTATGACAT 900
 QY 996 GCTTACATTTGCGAGTCTTCTGAGATGATTAAGAGACAGAGTCTCTGATTCAC 1055
 Db 901 GCTTACATTTGCGAGTCTTCTGAGATGATTAAGAGACAGAGTCTCTGATTCAC 960
 QY 1056 CTGAGACACAGTTCTGATGAGACAGTCTTAAGCCAGCGAGTCTGTGCTGCT 1115
 Db 961 CTGAGACACAGTTCTGATGAGACAGTCTTAAGCCAGCGAGTCTGTGCTGCT 1020
 QY 1116 ATCTCTCTTGAAGATGATGACACCTGATGATGATGATGATGATGATGATGAT 1175
 Db 1021 ATCTCTCTTGAAGATGATGACACCTGATGATGATGATGATGATGATGATGAT 1080
 QY 1176 CAAGACGACCCGCTCATGATGAGAGGACGATGCGCTCATCTTCAAGAGCCATGCT 1235
 Db 1081 CAAGACGACCCGCTCATGATGAGAGGACGATGCGCTCATCTTCAAGAGCCATGCT 1140
 QY 1236 GAGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1295
 Db 1141 GAGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
 QY 1296 TCGAATACACAGTGTGTTTCTGAGATGAGAGGAGATGATGATGATGATGATGAT 1355
 Db 1201 TCGAATACACAGTGTGTTTCTGAGATGAGAGGAGATGATGATGATGATGATGAT 1260


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Db      2121  GCCATCTCAGCCACCTATGCAACAAGCGGACGCTGCGACCTCCGCGCAACAGCGCCAG 2180
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DEFINITION Mus musculus axon guidance signal SEMA6A1 mRNA, complete cds.
ACCESSION AF288666
VERSION AF288666.1 GI:11093908
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

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REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCES
2 (bases 1 to 3018)
Klostermann, A., Iutz, B., Gertler, F. and Behl, C.
The orthologous human and murine semaphorin 6A-1 proteins
(SEMA6A-1/sem6A-1) bind to the enabled/vasodilator-stimulated
phosphoprotein-like protein (EVIL) via a novel carboxyl-terminal
zinc-like domain
J. Biol. Chem. 275 (50), 39647-39653 (2000)
20564339
10993894
2 (bases 1 to 3018)
Klostermann, A. and Behl, C.
Direct Submission
Submitted (21-JUL-2000) Independent Research Group
Neurodegeneration, MPI of Psychiatry, Kraepelinstrasse 2-10, Munich
80804, Germany
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Best Local Similarity 87.3%; Pred. No. 0;
Matches 2703; Conservative 0; Mismatches 312; Indels 81; Gaps 2;
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Db	961	TCCCATATATACCACAAACAAGAAAGGAGTGTTCGGAAAATTACTCCAAAGCCACGAC	1020
QY	1930	CAGCTGGTTCCCGTCAACCTCTTGGGCATTGTGACAGTCAACCTGGGCTTGTGATGGGGGCC	1989
Db	1021	CAGCTGGTTCCCGTCAACCTCTTGGGGCATGTGACGTATCTGGCTTGTCTCATGGGGGCC	1080
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QY	2290	CTGCAAGCAGAAAGCGGAAGCCAGCGCGGCGGACGCGCAGTGGGAGAGAGAACCGAAACCTC	2349
Db	1381	CTGCAAGCAGAAAGCGGAAGCCAGCGCGGCGGACGCGCAGTGGGAGAGAGAACCGAAACCTC	1440
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Db	1441	ATCAATGCTCTCACAAAGAGATGCCCCCATGGGCTTCCTGTGTATCCCAAGGACCTG	1500
QY	2410	CCCCGGGGGCTCCCCAGCCAAATCCCAAGCTGTGTGTGCTGCGCCATCAGCAGACAG	2469
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BASE COUNT 804 a 886 c 714 g 637 t
ORIGIN

Query Match 70.6%; Score 2182.4; DB 9; Length 3041;
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Matches 2183; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 VERSION AF030430.1
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 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 2770)
 Zhou, L., White, F.A., Lentz, S.I., Wright, D.E., Fisher, D.A. and
 Snider, W.D.
 Cloning and expression of a novel murine semaphorin with structural
 similarity to insect semaphorin 1
 Mol. Cell. Neurosci. 9 (1), 26-41 (1997)
 JOURNAL 97348468
 MEDLINE 2 (bases 1 to 2770)
 PUBMED 9204478
 REFERENCE Zhou, L.
 Direct Submission
 Submitted (17-OCT-1997) Neurology, Washington University, 660 S.
 JOURNAL Euclid Ave., St. Louis, MO 63110, USA
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BASE COUNT 720 a 735 c 701 g 614 t
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Best Local Similarity 88.9%; Pred. No. 0; Matches 2322; Conservative 0; Mismatches 286; Indels 3; Gaps 1;
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 BD157826
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 2293)
 Oca,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
 Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
 Primer for synthesizing full-length cDNA and use thereof
 Patent: JP 2002191363-A 12669 09-JUL-2002;
 JOURNAL
 HELIX RESEARCH INSTITUTE
 OS Homo sapiens (human)
 PN JP 2002191363-A/12669
 PD 09-JUL-2002
 PF 28-JUL-2000 JP 2000280990
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 PI SAITO,
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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

2 (bases 1 to 2293)
Isogai, T. and Otsuki, T.
Direct Submission
Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan: cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction; 5'- & 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

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DEFINITION	Primer for synthesizing full-length cDNA and use thereof.		
ACCESSION	BD127394		
VERSION	BD127394.1	GI:2822339	
KEYWORDS	JP 2002017375-A/2825		
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
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	Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,		
	Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and		
	Koga,H.		
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JOURNAL	OS. Homo sapiens (human)		
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Db 1741 ATAA 1744

RESULT 15
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LOCUS Homo sapiens cDNA FLJ90494 f1s, clone NT2RP3003614.
ACCESSION AK074975
VERSION AK074975.1 GI:22760768
KEYWORDS oligo capping; f1s (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T.,
Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S.,
Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y.,
Kojima,S., Nagahara,K., Masudo,Y., Ono,T., Okano,K., Yoshikawa,Y.,
Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and
Nishimura,K.
NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2227)

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AUTHORS Isogai,T. and Otsuki,T.
TITLE Direct Submission
JOURNAL Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction:
Institute of Medical Science, University of Tokyo; Laboratory of
Genome Structure, Human Genome Center; cDNA 5'-3'-end one pass
sequencing and clone selection: Helix Research Institute (supported
by Japan Key Technology Center etc.).
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ORIGIN
Query Match 56.3%; Score 1742.4; DB 9; Length 2227;
Best local similarity 99.9%; Pred. No. 0;
Matches 1743; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1 1TTGGCCAGAAATGAGAAATGAGTATGATGAGTGAAGCAAGCAAGATCATGGGCAT 120
QY 1410 TGTTCACACTCGAAATGACAGTATGATGAGTGAAGCAAGCAAGATCATGGGCAT 1469
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QY	2190	CAAGCTGGCCATCTCCGGGCAACACGGGCAAGATGCTATTAAGACAGACCAACCACT	2249
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QY	3030	ACCCCCCAACCACTCTTTGCTCCCCCTTCCACATCCATCCATGAAGCCCAATGATGGGTATAC	3089
Db	1681	ACCCCCCAACCACTCTTTGCTCCCCCTTCCACATCCATGAAGCCCAATGATGGGTATAC	1740
QY	3090	ATAA 3093	
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Job time : 11088.7 secs

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PD 02-JUN-2000.
 XX 26-NOV-1999; 99WO-EP09215.
 XX 26-NOV-1998; 98EP-0122441.
 PR (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 PA Behl C, Klostermann A;
 PI MPI: 2000-400065/34.
 DR P-PSDB: AA771460.
 XX Nucleic acid coding for human semaphorin 6A-1 used as diagnostic agent,
 PT therapeutic agent, for modulating immune system, in gene therapy or for
 PT effecting differentiation, cytoskeletal stabilization and/or plasticity
 PT -
 PS Claim 1; Fig 2; 53pp; English.
 XX The present sequence is a cDNA encoding transmembranous human semaphorin
 CC 6A-1 ((HSA)SEMA6A-1) which is involved in neuronal development and
 CC regeneration mechanisms during apoptosis. Semaphorin is a family of
 CC proteins displaying secreted or transmembrane-based repulsive guidance
 CC cues critically involved in neuronal development. The present sequence
 CC was isolated from human 1-ZAP Express cDNA library which was screened
 CC using a PCR fragment amplified from human neuroblastoma cell line
 CC SK-N-MC cDNA. The (HSA)SEMA6A-1 protein contains a zyxin-like domain
 CC that selectively binds to members of Ena/VASP protein family especially
 CC Evi1. Expression of (HSA)SEMA6A-1 is highest in embryonic brain and
 CC kidney and moderate in lung. The present sequence is useful as diagnostic
 CC and therapeutic agents, for modulating the immune system, in gene
 CC therapy, for effecting differentiation, cytoskeletal stabilisation
 CC and plasticity.
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 Matches 3093; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 3238 AGCAAGATCCCAACCATGAGGATGAACTTGTGAGAACTGGAACGCTGCCGCCAAA 3297
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RESULT 2
 AAA93617
 ID AAA93617 standard; DNA; 3498 BP.
 AC AAA93617;
 XX
 AC 16-JAN-2001 (first entry)
 DT
 XX
 DE Human semaphorin protein-like splice variant SECX 2864933-1 DNA.
 XX
 KW SFXC protein; human; secreted; membrane-associated; cancer;
 KW proliferation regulator; differentiation regulator; non-malignant tumour;
 KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
 KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
 KW skin disorder; cardiovascular disorder; atherosclerosis; stenosis;
 KW neurological disease; Alzheimer's disease; trauma; wounding;
 KW spinal cord injury; skeletal disorder; cytoskeletal; immunosuppressive;
 KW anti-HIV; anti-inflammatory; antiatherosclerotic;
 KW neuroprotective; vulnerable; antiallergic; antimicrobial; cardiant;
 KW dermatological; gene therapy; ds.
 OS
 XX
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 XX
 PN W0200053742-A2.
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 PD 14-SEP-2000.
 XX
 PF 09-MAR-2000; 2000MO-US06280.
 XX
 PR 09-MAR-1999; 99US-0123667.
 PR 08-MAR-2000; 2000US-0123667.
 XX
 PA (CURA-) CURAGEN CORP.
 PA
 PI Shinketsu RA;
 XX
 XX WPI: 2000-594318/56.
 DR P-PSDB; AAB23030.
 XX
 PT Novel human membrane associated or secreted polypeptides and
 PT polynucleotides useful for diagnosis, prevention and treatment of
 PT pathological states such as cancer, immune, cardiovascular and

PT neurological disorders -
 XX
 XX Claim 3; Fig 2; 151pp; English.

CC Sequences AAA93616-A93631 and AAA93673-A93676 represent nucleic acids
 CC which encode human SECX proteins (AA933029-B23048). The SECX proteins
 CC of the invention are either secreted or membrane-associated proteins
 CC and act as regulator of cellular proliferation and differentiation. SECX
 CC proteins or nucleotides are useful for diagnosing the presence of, or
 CC predisposition to, a disease associated with altered levels of SECX
 CC proteins and nucleotides. The SECX proteins are also useful to screen
 CC compounds that modulate SECX activity or expression. The interaction of
 CC a SECX protein with other cellular proteins may be useful to modulate
 CC the activity of a partner protein, cellular proliferation, cellular
 CC differentiation and cell survival. SECX nucleotides are useful for the
 CC recombinant expression of SECX protein, and may be used to detect SECX mRNA
 CC or genetic lesions in the SECX gene. They may also be used to modulate
 CC SECX expression (e.g., using antisense oligonucleotides). SECX nucleic
 CC acid sequences are also useful for identifying a cell or tissue type in
 CC a biological sample, and in forensic biology. SECX primers or probes are
 CC useful for detecting the presence of SECX nucleotides and for screening
 CC tissue cultures for contamination. Diseases that may be treated or
 CC prevented using SECX proteins or nucleotides include cancer (e.g.,
 CC colorectal carcinoma, prostate cancer), benign tumors, immune disorders
 CC (including autoimmune diseases, transplant rejection, allergies, AIDS),
 CC infections, inflammatory disorders, arthritis, hematopoietic disorders,
 CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,
 CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g.,
 CC surgical or traumatic wounds, spinal cord injury), and skeletal
 CC disorders.

XX
 CC Sequence 3498 BP; 917 A; 966 C; 889 G; 725 T; 1 other;

Query Match 98.2%; Score 3038; DB 21; Length 3498;
 Best Local Similarity 99.3%; Pred No. 0;

Matches 3072; Conservative 0; Mismatches 21; Indels 2; Gaps 2;

QY 1 ATGAGTCAAGAGCCTTCTCTATATTTACACTGCTACACTTTGCTGGGCTGGTTTC 60
 DB 214 ATGAGTCAAGAGCCTTCTCTATATTTACACTGCTACACTTTGCTGGGCTGGTTTC 273
 QY 61 CCAGAGATTTGAGCCATTCAGTATTTGGCATGGCACTATACAAAAGATCCGGTG 120
 DB 274 CCAGAGATTTGAGCCATTCAGTATTTGGCATGGCACTATACAAAAGATCCGGTG 333
 QY 121 TTGTGGCCACAAGCCAGGAGGAAACACACACAGAGGACAGGCTGACATCCAGATG 180
 DB 334 TTGTGGCCACAAGCCAGGAGGAAACACACACAGAGGACAGGCTGACATCCAGATG 393
 QY 181 ATTATGATCATAGAGGAAACCTCTACATTTGCTGAGGACCAATTTATCTGTGAT 240
 DB 394 ATTATGATCATAGAGGAAACCTCTACATTTGCTGAGGACCAATTTATCTGTGAT 453
 QY 241 ATAGACATCAACACGGAAGAAATTTATAGCAAAAACCTGATGGAATCTAA 300
 DB 454 ATAGACATCAACACGGAAGAAATTTATAGCAAAAACCTGATGGAATCTAA 513
 QY 301 CAGGCGATGTAGACATGCAAGATGAAGGAAAAACATPAAGATAGTGCACAACCTT 360
 DB 514 CAGGCGATGTAGACATGCAAGATGAAGGAAAAACATPAAGATAGTGCACAACCTT 573
 QY 361 ATTAAGTCTTCTAAAGAAAAACGATGATGCTTTGCTGAGCACTATGCTTC 420
 DB 574 ATTAAGTCTTCTAAAGAAAAACGATGATGCTTTGCTGAGCACTATGCTTC 633
 QY 421 AACCCCTCTGCGAAGAACTATAAGATGATGATGATGATGATGATGATGATGATGAT 480
 DB 634 AACCCCTCTGCGAAGAACTATAAGATGATGATGATGATGATGATGATGATGATGAT 693
 QY 481 GGAATGGCAGATGCCATATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 DB 694 GGAATGGCAGATGCCATATGATGATGATGATGATGATGATGATGATGATGATGAT 753

QY 541 AAACATACCTGACGACAGTGAATGATCTTCTTCCATTTAGCAGATCATTTACCGAGT 600
 DB 754 AAACATACCTGACGACAGTGAATGATCTTCTTCCATTTAGCAGATCATTTACCGAGT 813
 QY 601 CTGGAGAAAGCCCTTACCTGCGACCCGTCAGACAGATTCAAATTTGTTGAAAGACCA 660
 DB 814 CTGGAGAAAGCCCTTACCTGCGACCCGTCAGACAGATTCAAATTTGTTGAAAGACCA 873
 QY 661 TACTTTGTTCAAGCCGTGATAGAGATTAATCTTCTTCTTCCAGGAAATAGCA 720
 DB 874 TACTTTGTTCAAGCCGTGATAGAGATTAATCTTCTTCTTCCAGGAAATAGCA 933
 QY 721 GTGAGATTAACACCATGGGAAAGTAGTTTCCCAAGAGTGGCTCAGTTTGTAAAGAT 780
 DB 934 GTGAGATTAACACCATGGGAAAGTAGTTTCCCAAGAGTGGCTCAGTTTGTAAAGAT 993
 QY 781 GATATGGGAGATTCACAAAGATCTCTGAGAAACAGTGGACGCTCTGAAAGGGGAC 840
 DB 994 GATATGGGAGATTCACAAAGATCTCTGAGAAACAGTGGACGCTCTGAAAGGGGAC 1053
 QY 841 TTGAACGCTCAGTCTGAGACCTCTCATTTTATTTTCAACATTTCTCCAGCAGTTTACA 900
 DB 1054 TTGAACGCTCAGTCTGAGACCTCTCATTTTATTTTCAACATTTCTCCAGCAGTTTACA 1113
 QY 901 GATGATTCGATACAGGCGGCTGATGTTGCTGCGAACGTTTCTACACTTTATAC 960
 DB 1114 GATGATTCGATACAGGCGGCTGATGTTGCTGCGAACGTTTCTACACTTTATAC 1173
 QY 961 AGCATCCCGGGGCTGCGACGCTGCTGCTTACATCTGACATCTGACATCTGACATCTTACT 1020
 DB 1174 AGCATCCCGGGGCTGCGACGCTGCTGCTTACATCTGACATCTGACATCTGACATCTTACT 1233
 QY 1021 GGGAGATTCAGAGACAGAGATCTCTGATTCACACCTGACACACATCTCTGATAGCA 1080
 DB 1234 GGGAGATTCAGAGACAGAGATCTCTGATTCACACCTGACACACATCTCTGATAGCA 1293
 QY 1081 GTTCTTAAGCCAGGCGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
 DB 1294 GTTCTTAAGCCAGGCGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1353
 QY 1141 TCCAAATGATCCCTGATATACCTGATCAATCAACAGCAGCCGCTCATGATGATG 1200
 DB 1354 TCCAAATGATCCCTGATATACCTGATCAATCAACAGCAGCCGCTCATGATGATG 1413
 QY 1201 GCAATGCCCTCATCTTCAACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
 DB 1414 GCAATGCCCTCATCTTCAACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1473
 QY 1261 ACCAAATTTGAGTGGACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
 DB 1474 ACCAAATTTGAGTGGACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1533
 QY 1321 GGATCAGAGAGGAAATCATCTTGAATTTTGGCCAGAAATAGAAATAGTGTCTTCTA 1380
 DB 1534 GGATCAGAGAGGAAATCATCTTGAATTTTGGCCAGAAATAGAAATAGTGTCTTCTA 1593
 QY 1381 AATGACAGCTTTTCTGAGAGAGATGATGATTAACCTGAAATTAAGCACTATGAT 1440
 DB 1594 AATGACAGCTTTTCTGAGAGAGATGATGATTAACCTGAAATTAAGCACTATGAT 1653
 QY 1441 GGAATGAGACAAAAGATTCATGAGGATGACAGTGGACAGCAAGCAGCTCTGTAT 1500
 DB 1654 GGAATGAGACAAAAGATTCATGAGGATGACAGTGGACAGCAAGCAGCTCTGTAT 1713
 QY 1501 GTTGGCTTCTACCTGCTGATTAAGGTTTCCCTTGGCGGTGTGACAGCACTTGGGAG 1560
 DB 1714 GTTGGCTTCTACCTGCTGATTAAGGTTTCCCTTGGCGGTGTGACAGCACTTGGGAG 1773
 QY 1561 TGTAAATAAACCTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
 DB 1774 TGTAAATAAACCTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1833
 QY 1621 GCTCAGGCAATTTATCACCCACAGCAGCTGCTTTGAGCAGGACATAGACCGTGGC 1680

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Db      1834  GCGTCAGACATTATACACCCACAGACACTGACTTTGAGAGGACATAGAGCGGTGC 1893
QY      1681  AATACAGATGCTGTGGGGAGCTGTCAATTCCTTTGTGCACTGATGGGCAATTCAGT 1740
Db      1894  AATACAGATGCTGTGGGGAGCTGTCAATTCCTTTGTGCACTGATGGGCAATTCAGT 1953
QY      1741  TCCCTCTGCCAGCAGCAACACATCAGATTGCGAGGCTCAGAGGGGATATGAGTACG 1800
Db      1954  TCCCTCTGCCAGCAGCAACACATCAGATTGCGAGGCTCAGAGGGGATATGAGTACG 2013
QY      1801  GAGGAGATGCTGAGTGTGGAAGCTGTGCTTGAATCTGACAGCAGCAGACACCTTTGG 1860
Db      2014  GAGGAGATGCTGAGTGTGGAAGCTGTGCTTGAATCTGACAGCAGCAGACCTTTGG 2073
QY      1861  GCAGTCTTCCATATATCCAAAGAGAGAGAGGATGATGGGAAAGTACTCTCAAA 1920
Db      2074  GCAGTCTTCCATATATCCAAAGAGAGAGAGGATGATGGGAAAGTACTCTCAAA 2133
QY      1921  GAGCAGAGACAGCTGTGCTCCGCTACCCCTTGGCCATGTCAGTCACTGCTTTCGTC 1980
Db      2134  GAGCAGAGACAGCTGTGCTCCGCTACCCCTTGGCCATGTCAGTCACTGCTTTCGTC 2193
QY      1981  ATGGGGGCGCTCTTTCGAGCATACCCGCTACTGGCTGTGATCACTGGGCGGAAAGAC 2040
Db      2194  ATGGGGGCGCTCTTTCGAGCATACCCGCTACTGGCTGTGATCACTGGGCGGAAAGAC 2253
QY      2041  GTGGCTGTGTGTCAGGCGCAAGAGAGAGAGTCAACCCACTGCGGCGGCTCCATGAGC 2100
Db      2254  GTGGCTGTGTGTCAGGCGCAAGAGAGAGAGTCAACCCACTGCGGCGGCTCCATGAGC 2313
QY      2101  AGCGTCAACCAAGCTCAGCGGCTCTTGTGGGACACTCAATCCAAAGACCCAAAGCCGAG 2160
Db      2314  AGCGTCAACCAAGCTCAGCGGCTCTTGTGGGACACTCAATCCAAAGACCCAAAGCCGAG 2373
QY      2161  GCCATCTCTCAAGCCACTATGCAACAAGGCAAGTGGCCACTCCCGGCAACAGGCGCAAG 2220
Db      2374  GCCATCTCTCAAGCCACTATGCAACAAGGCAAGTGGCCACTCCCGGCAACAGGCGCAAG 2433
QY      2221  ATGTCTAATTAAGAGAGACAGCAGCAGCTGAGTGAAGGCGCTCCACACCCAGAGTCA 2280
Db      2434  ATGTCTAATTAAGAGAGACAGCAGCAGCTGAGTGAAGGCGCTCCACACCCAGAGTCA 2493
QY      2281  ACCCCAAAGCTGACGAGAAAGCGGAGCCAGCCGCGGAGCCGAGTGGAGAGAGAAC 2340
Db      2494  ACCCCAAAGCTGACGAGAAAGCGGAGCCAGCCGCGGAGCCGAGTGGAGAGAGAAC 2553
QY      2341  CAGAACTCATCAATGCTGTGACAAAGAGACATGCCGCCCATGGGCTCCCTGTGATTCCC 2400
Db      2554  CAGAACTCATCAATGCTGTGACAAAGAGACATGCCGCCCATGGGCTCCCTGTGATTCCC 2613
QY      2401  ACGGACTGCGCCCTGCGGGGCTTCCCGCAGCAGCATCCAGCTGTGATGCTCCCATC 2460
Db      2614  ACGGACTGCGCCCTGCGGGGCTTCCCGCAGCAGCATCCAGCTGTGATGCTCCCATC 2673
QY      2461  ACGCAGCAGGAGGCTACAGCATGAGTGTGAGCAAGCCCAAAATGAGGAGGTGGCCAG 2520
Db      2674  ACGCAGCAGGAGGCTACAGCATGAGTGTGAGCAAGCCCAAAATGAGGAGGTGGCCAG 2733
QY      2521  ATGGCGCTGTGAGAGACAGGCGCCACACTGAGTATAGACATCAAGAGAGATCTGAGC 2580
Db      2734  ATGGCGCTGTGAGAGACAGGCGCCACACTGAGTATAGACATCAAGAGAGATCTGAGC 2793
QY      2581  AGCAAGAGTCCCAACCATGAGGCTGTGAGCAAGCTGTGAGCAAGCTGTGAGCAAG 2640
Db      2794  AGCAAGAGTCCCAACCATGAGGCTGTGAGCAAGCTGTGAGCAAGCTGTGAGCAAG 2853
QY      2641  GTTCACACGCGGAGGCTCTCCCTGGGTCGCCCGGAGAGCTCTCCCTGTCAAGCGGTCTA 2700
Db      2854  GTTCACACGCGGAGGCTCTCCCTGGGTCGCCCGGAGAGCTCTCCCTGTCAAGCGGTCTA 2913
QY      2701  AGCAAGGCGCTGTGAGAGTCAAGTCCCTCTCTACAGGAGGTGATATAGAGAGCTAC 2760

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Db      2914  AGCAAGGCGCTGTGAGAGTCAAGTCCCTCTCTCTACAGGAGGTGACTATAGAGAGCTAC 2973
QY      2761  CCCAGCACTGCTCTACGAGAGAGCCACAGGCGCAC- ACTCTGAAAAAGAAACACTAA 2819
Db      2974  CCCAGCACTGCTCTACGAGAGAGCCACAGGCGCAC- ACTCTGAAAAAGAAACACTAA 3033
QY      2820  CTCCTCCATCTCTCTC- ACCTCTCGAGAAACAGAGCTTTGGCAGGGGAGACACCGCG 2878
Db      3034  CCCGACAAATTCATCTGACTTCAAAAGGAGCAGAGCTTTGGCAGGGGAGACACCGCG 3093
QY      2879  CGCCGCGCGCGAGAGGGTGTGACTCCATCCAGGTGACACAGCTCCAGCCTCTGCGCAG 2938
Db      3094  CGCCGCGCGCGAGAGGGTGTGACTCCATCCAGGTGACACAGCTCCAGCCTCTGCGCAG 3153
QY      2939  CGGTGACTGTCTGAGAGGAGCCACAGCTCTAAAGCTTAACACTACTATACAGAGTGGGG 2998
Db      3154  CGGTGACTGTCTGAGAGGAGCCACAGCTCTAAAGCTTAACACTACTATACAGAGTGGGG 3213
QY      2999  TGAAGGTAGCGCCCTGCTAAAGCGGAGAGTACCCCAACCATCTTGTCTCCCTTT 3058
Db      3214  TGAAGGTAGCGCCCTGCTAAAGCGGAGAGTACCCCAACCATCTTGTCTCCCTTT 3273
QY      3059  CCACATCCATGAAGCCCAATGATGCGGTACATTA 3093
Db      3274  CCACATCCATGAAGCCCAATGATGCGGTACATTA 3308

RESULT 3
ABX71103
ID  ABX71103 standard; cDNA; 4280 BP.
AC  ABX71103;
DE  05-MAR-2003 (first entry)
XX  Novel human cDNA sequence #328.
DE  Novel human cDNA sequence #328.
KW  Human; gene; ss; nervous system disorder; peripheral neuropathy;
KW  Huntington's disease; amyotrophic lateral sclerosis; haemophilia;
KW  neurodegenerative disease; Parkinson's disease; Alzheimer's disease;
KW  autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis;
KW  insulin-dependent diabetes mellitus; anaemia; thrombocytopenia; wound;
KW  ulcer; burn; bone disorder; osteoporosis; osteoarthritis; stroke;
KW  fibrosis; reperfusion injury; infection; allergic rhinitis; asthma;
KW  coagulation disorder; cancer; tumour; inflammation; chemotactic;
KW  septic shock; Crohn's disease; anaphylaxis; proliferation;
KW  differentiation; stem cell growth factor; haematopoiesis; chemokinetic;
KW  haemostatic; antiinflammatory; expressed sequence tag; EST.
OS  Homo sapiens.
XX  Homo sapiens.
XX  WO200281731-A2.
XX  17-OCT-2002.
XX  29-JAN-2002; 2002WO-US01222.
XX  30-JAN-2001; 2001US-0774528.
XX  (HYSE-) HYSEQ INC.
XX  (GOOD/) GOODRICH R W.
XX  Tang TY, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
XX  Xue AJ, Yang Y, Wehrman T, Wang J, Wang D, Dmanac RT;
XX  WPI; 2003-058563/05.
XX  Novel polypeptide useful for treating neurodegenerative diseases,
XX  myeloid or lymphoid cell disorders, bone disorders, mechanical and
XX  traumatic disorders, coagulation disorders, and inflammatory diseases
XX  Claim 1; Page -; 612pp; English.

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XX This invention relates to the cDNA sequences encoding an isolated novel human polypeptide. The protein encoded by the nucleic acid of the invention is useful for treating central and peripheral nervous system diseases (e.g., peripheral neuropathy, Huntington's disease, amyotrophic lateral sclerosis); neurodegenerative diseases (e.g., Parkinson's disease, Alzheimer's disease); autoimmune disease (e.g., systemic lupus erythematosus, rheumatoid arthritis, insulin-dependent diabetes mellitus); myeloid or lymphoid cell disorders (e.g., anemia and thrombocytopenia); wounds, ulcers, burns; bone disorders (e.g., osteoporosis, osteoarthritis); mechanical and traumatic disorders (e.g., stroke, head trauma); lung or liver fibrosis; reperfusion injury in various tissues; bacterial, viral or fungal infections; allergic conditions such as allergic rhinitis, asthma; coagulation disorders (e.g., hemophilia); cancer and tumors; and inflammatory diseases (e.g., septic shock, Crohn's disease, anaphylaxis). The protein may be used to inhibit the growth, infection or function of infectious agents such as bacteria, fungi, viruses, or to effect bodily characteristics, CC biohythms or circadian cycles of rhythms. The protein may also have proliferation/differentiation, stem cell growth factor, CC haematopoiesis regulation, immune stimulating or suppressing, CC chemotactic/chemokinetic, hemostatic and thrombolytic receptor/ligand, CC and antiinflammatory activities. The cDNA sequences of the invention are useful for expressing recombinant protein for analysis. The present CC sequence represents a novel human cDNA sequence of the invention, CC this sequence is an expressed sequence tag (EST) and was identified CC using subtractive hybridisation.

XX Sequence 4280 BP; 1185 A; 1165 C; 1001 G; 929 T; 0 other;

Query Match 98.0%; Score 3032; DB 25; Length 4280;

Best Local Similarity 98.4%; Pred. No. 0;

Matches 3093; Conservative 0; Mismatches 0; Indels 51; Gaps 1;

QY 1 ATGAGGTGAGAGCCCTTCTGCTATATTTTCACTCTACCTTCTGGGCTGGTTTC 60
DB 267 ATGAGGTGAGAGCCCTTCTGCTATATTTTCACTCTACCTTCTGGGCTGGTTTC 326
QY 61 CCGAGAGATTCGAGCAATCACTATTTGCGATGGAGCACTATCAAAACAGTATCCGGT 120
DB 327 CCGAGAGATTCGAGCAATCACTATTTGCGATGGAGCACTATCAAAACAGTATCCGGT 386
QY 121 TTTGTGGGCCAAGCCAGGAGCAACACCAACAGAGGCGACAGGCTGGATCCAGATG 180
DB 387 TTTGTGGGCCAAGCCAGGAGCAACACCAACAGAGGCGACAGGCTGGATCCAGATG 446
QY 181 ATTATGATCATGAGGAAACCTCTCATTTGCTGAGGAGCACTATTTTACTGTTGAT 240
DB 447 ATTATGATCATGAGGAAACCTCTCATTTGCTGAGGAGCACTATTTTACTGTTGAT 506
QY 241 ATGAGACATCACACAGGAGAAATTTATGTAGCAAAAACGTGACATGGAATCTAGA 300
DB 507 ATGAGACATCACACAGGAGAAATTTATGTAGCAAAAACGTGACATGGAATCTAGA 566
QY 301 CAGGCCGATGTAGACATCGAGATGAGAGGAAACATTAAGATGATGCCACACTTT 360
DB 567 CAGGCCGATGTAGACATCGAGATGAGAGGAAACATTAAGATGATGCCACACTTT 626
QY 361 ATTAAAGTTCTTAAAGAAAAGAGATGATGATTTGTTGCTGTGAACTAATGCCCTTC 420
DB 627 ATTAAAGTTCTTAAAGAAAAGAGATGATGATTTGTTGCTGTGAACTAATGCCCTTC 686
QY 421 AACCCCTGTCGACAAACTATAGATGATGATGGAACCATTCGGGGATGATTTGAGC 480
DB 687 AACCCCTGTCGACAAACTATAGATGATGATGGAACCATTCGGGGATGATTTGAGC 746
QY 481 GGAATGCGCAGATGCCATATGATGCCAAACATGCCAAGCTTGCATGTTTGCAGATGA 540
DB 747 GGAATGCGCAGATGCCATATGATGCCAAGCTTGCATGTTTGCAGATGA 806
QY 541 AAACATATCTAGCAGCAGTACTGATCTTCTGCAATGACGAGCATTTACCGAGGT 600
DB 807 AAACATATCTAGCAGCAGTACTGATCTTCTGCAATGACGAGCATTTACCGAGGT 866

QY 601 CTGGAGAAAGCCCTTACCTCGGACCTGCAAGCAGATTCAAATGTTGAAAGACCA 660
DB 867 CTGGAGAAAGCCCTTACCTCGGACCTGCAAGCAGATTCAAATGTTGAAAGACCA 926
QY 661 TACTTGTTCAGCCGCTGATTTACGAGATTTATCTCTCTTTTCAAGGAATATACA 720
DB 927 TACTTGTTCAGCCGCTGATTTACGAGATTTATCTCTCTTTTCAAGGAATATACA 986
QY 721 GTGGAGTATTAACCATGAGGAAAGTAGTTTCCCAAGAGTGGCTCAGGTTTGAAGAT 780
DB 987 GTGGAGTATTAACCATGAGGAAAGTAGTTTCCCAAGAGTGGCTCAGGTTTGAAGAT 1046
QY 781 GATATGGAGATTCGAAAGAGTCTGAGAAACAGTGAACGCTGTTCTGAAGCGCC 840
DB 1047 GATATGGAGATTCGAAAGAGTCTGAGAAACAGTGAACGCTGTTCTGAAGCGCC 1106
QY 841 TTGAACCTGCTAGTTCTGAGACCTCTATTTTATTCACATTCCTCAGGAGTTACA 900
DB 1107 TTGAACCTGCTAGTTCTGAGACCTCTATTTTATTCACATTCCTCAGGAGTTACA 1166
QY 901 GATGATTCGATACAGCGGCGTATGTTGCTGCGCAAGCTTTCTACACCTTATAC 960
DB 1167 GATGATTCGATACAGCGGCGTATGTTGCTGCGCAAGCTTTCTACACCTTATAC 1226
QY 961 AGCATCCCTGGCTGCTGCACTCTGCTGATGACATCTTGACATTCGCCAGTGTCTACT 1020
DB 1227 AGCATCCCTGGCTGCTGCACTCTGCTGATGACATCTTGACATTCGCCAGTGTCTACT 1286
QY 1021 GGGAGATTCAGAGAAAGAGAGTCTGATTCACCTGAGACACCACTTCTGATGAACGA 1080
DB 1287 GGGAGATTCAGAGAAAGAGAGTCTGATTCACCTGAGACACCACTTCTGATGAACGA 1346
QY 1081 GTTCTTAAGCCCGAGGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1347 GTTCTTAAGCCCGAGGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1406
QY 1141 TCCATGAGTTCCTCTGATGATACCTGATGATACATGATGATGATGATGATGATGAT 1200
DB 1407 TCCATGAGTTCCTCTGATGATACCTGATGATACATGATGATGATGATGATGATGAT 1466
QY 1201 GCAGTGGCTCCATCTCTCAACAGGCAATGTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
DB 1467 GCAGTGGCTCCATCTCTCAACAGGCAATGTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1526
QY 1261 ACCAAATTTGCACTGACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1527 ACCAAATTTGCACTGACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1386
QY 1321 GATGACAGAAAGGAATCATCTGGAATTTTGGCCAGATGAGAAATAGTGTCTCTA 1380
DB 1587 GATGACAGAAAGGAATCATCTGGAATTTTGGCCAGATGAGAAATAGTGTCTCTA 1646
QY 1381 AATGACAGCTTTTCTGAGAGATGATGTTTACAACCTGTAAGAAATGACGATGAT 1440
DB 1647 AATGACAGCTTTTCTGAGAGATGATGTTTACAACCTGTAAGAAATGACGATGAT 1706
QY 1441 GGAATGAGAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
DB 1707 GGAATGAGAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1766
QY 1501 GTTCTGCTTCTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
DB 1767 GTTCTGCTTCTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1826
QY 1561 TGTAAAAAAGCTTATGCTCCAGAGACCATATGTTGATGATGATGATGATGATGATGAT 1620
DB 1827 TGTAAAAAAGCTTATGCTCCAGAGACCATATGTTGATGATGATGATGATGATGATGAT 1886
QY 1621 GCTGACAGCAATTTATACCCAGAGAGATGATGATGATGATGATGATGATGATGATGAT 1680
DB 1887 GCTGACAGCAATTTATACCCAGAGAGATGATGATGATGATGATGATGATGATGATGAT 1946

QY	1681	AAATACGATGAGTCTGGGGGGAGCTGTCCAAATTCCTTTGTGGCACTGA-----	1726
Db	1947	AAATACGATGAGTCTGGGGGGAGCTGTCCAAATTCCTTTGTGGCACTGAATTCATTTCACT	2006
QY	1727	-----ATGGGCAATTCAGTTCCTCTTG	1749
Db	2007	CCTCTACGACATTAATGAATGCTTTTACAAACAGGTGATGGGATTTCAGTTCCCTCTTG	2066
QY	1750	CCGACGACAACCAATCAGATTCGACGGCTCAAGAGGGGTATGATCTAGGGAGGAATG	1809
Db	2067	CCGACGACAACCAATCAGATTCGACGGCTCAAGAGGGGTATGATCTAGGGAGGAATG	2126
QY	1810	CTGAGCTGGGAAGATCTGCTTGACTCACTCGAAGACACAGACCCCTTTGGGGGAGAGTCT	1869
Db	2127	CTGAGCTGGGAAGATCTGCTTGACTCACTCGAAGACACAGACCCCTTTGGGGGAGAGTCT	2186
QY	1870	TCCCATATATACCAAGACAGAAAGGAGAGTATTCGGGAAAGTTATACCTCAAAAGGCCAGAC	1929
Db	2187	TCCCATATATACCAAGACAGAAAGGAGAGTATTCGGGAAAGTTATACCTCAAAAGGCCAGAC	2246
QY	1930	CAGCTGGTCCCGTCAACCCCTCTTTGGCCATTGCAATCTCTGGCTTTGTCATG666GCC	1989
Db	2247	CAGCTGGTCCCGTCAACCCCTCTTTGGCCATTGCAATCTCTGGCTTTGTCATG666GCC	2306
QY	1990	GTCCTCTCGGGGCATCAACCGTCTACTGGTGTGATCATG666GCAAAAGCGGGCTGTG	2049
Db	2307	GTCCTCTCGGGGCATCAACCGTCTACTGGTGTGATCATG666GCAAAAGCGGGCTGTG	2366
QY	2050	GTCGACGCGCAAGGAGAGAGGAGCTACCCATCTCCGCGCGGCGGCTCAATGACACAGCTACG	2109
Db	2367	GTCGACGCGCAAGGAGAGAGGAGCTACCCATCTCCGCGCGGCGGCTCAATGACACAGCTACG	2426
QY	2110	AAAGCTAGCGGCTCTTTGGGGAOACTCAATCCAAAGACCCAAAGCCGAGGCCATCTC	2169
Db	2427	AAAGCTAGCGGCTCTTTGGGGAOACTCAATCCAAAGACCCAAAGCCGAGGCCATCTC	2486
QY	2170	ACGCACTCATGCAACAACGGCAAGCTGCCCATCTCCGGCAACAAGGCCAGATGTCATTT	2229
Db	2487	ACGCACTCATGCAACAACGGCAAGCTGCCCATCTCCGGCAACAAGGCCAGATGTCATTT	2546
QY	2230	AAACCAACCAAGCAACCACTGGAGCTGACGGCCCTCCCAACCCAGATCAACCCCAAGC	2289
Db	2547	AAACCAACCAAGCAACCACTGGAGCTGACGGCCCTCCCAACCCAGATCAACCCCAAGC	2606
QY	2290	CTGAGAGCAAGCGGAGAGCCAGCGCGCGGACGCGCAGTGTGGAGAGAAACAGAACTC	2349
Db	2607	CTGAGAGCAAGCGGAGAGCCAGCGCGCGGACGCGCAGTGTGGAGAGAAACAGAACTC	2666
QY	2350	ATCATATGCTGTACAAAGGACATGCCCCCCTATGGGCTCCCTGTGATTTCCACGAGACTG	2409
Db	2667	ATCATATGCTGTACAAAGGACATGCCCCCCTATGGGCTCCCTGTGATTTCCACGAGACTG	2726
QY	2410	CCCCCTGGGGGCTCCCCAGCAATCCCAAGCTGGTGGTCTGCGCCATCACACAGACAG	2469
Db	2727	CCCCCTGGGGGCTCCCCAGCAATCCCAAGCTGGTGGTCTGCGCCATCACACAGACAG	2786
QY	2470	GGCTACCAAGCATGAGTACGTGGACACCCAAAATGAAGCAAGTGTGGCCAGATGGCGTGTG	2529
Db	2787	GGCTACCAAGCATGAGTACGTGGACACCCAAAATGAAGCAAGTGTGGCCAGATGGCGTGTG	2846
QY	2530	GAGAGCAAGGCTCCGCAACTGTGAGTATTAAGACCATCAAGAGAACTCTCAGAGCAAGAT	2589
Db	2847	GAGAGCAAGGCTCCGCAACTGTGAGTATTAAGACCATCAAGAGAACTCTCAGAGCAAGAT	2906
QY	2590	CCCAACAATGGGGTGAACCTGTGAGAGAACTGGACAGCTCGCCCCCAAGTTCCACAG	2649
Db	2907	CCCAACAATGGGGTGAACCTGTGAGAGAACTGGACAGCTCGCCCCCAAGTTCCACAG	2966
QY	2650	CGGGAGGAGCTCCCTGGGGTCCCCCGGGAACCTCCCTGCTCAGACCGGCTTAAGCAAGCGG	2709
Db	2967	CGGGAGGAGCTCCCTGGGGTCCCCCGGGAACCTCCCTGCTCAGACCGGCTTAAGCAAGCGG	3026
QY	2710	CTGGAATGACACACTCTCTTTCTACGGGGTGTGACTTAAGAGAGCTACCCACAGAC	2765

Db	3027	CTGGAAATGACCACTCCTCTTCTCTAGGGGTTGACTATAAGAGAGCTACCCACGAAAC	3086
QY	2770	TCGCTCAGAGAGACCCACCGGCCACCACTGTCAAAAAGAAACACACTTAATCTCTCAAT	2829
Db	3087	TCGCTCAGAAACCCACACGAGCCACCACTGTCAAAAAGAAACACACTTAATCTCTCAAT	3146
QY	2830	TCCTCTCAACCTCTCCAGAAACACAGAGCTTTGGCAGGGGAGACAACCCGCCGCCGCCG	2883
Db	3147	TCCTCTCAACCTCTCCAGAAACCAAGCTTTGGCAGGGGAGACAACCCGCCGCCGCCG	3200
QY	2890	CAGAGGGTGAGCTCCATCTCCAGGTGCACACGCTCCACGCCATTTGGCCAGGCGGTACTGT	2944
Db	3207	CAGAGGGGTGAGCTCCATCTCCAGGTGCACACGCTCCACGCCATTTGGCCAGGCGGTACTGT	3266
QY	2950	TCGAGGACAGCCCAACGCTTAACGCTTACAACTCAGTCAGCAAGGTGCGGGCTGAAGGCTACG	3005
Db	3267	TCGAGGACAGCCCAACGCTTACGCTTACAACTCAGTCAGCAAGGTGCGGGCTGAAGGCTACG	3322
QY	3010	CCCTCGCTAAAGCCGAGCTACCCCCCAACCATCTCTTGGCTCCCTTTCCACATCCATG	3065
Db	3327	CCCTCGCTAAAGCCGAGCTACCCCCCAACCATCTCTTGGCTCCCTTTCCACATCCATG	3386
QY	3070	AAGCCCAATGATGGGTGACTAA	3093
Db	3387	AAGCCCAATGATGGGTGACTAA	3410

RESULT 4
 AAH18729
 ID AAH18729 standard; cDNA; 6060 BP.
 XX
 AC AAH18729;
 XX
 DT 26-JUN-2001 (first entry)
 XX
 DE Human cDNA sequence SEQ ID NO:19004.
 XX
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1074617-A2.
 XX
 PD 07-FEB-2001.
 XX
 PF 28-JUL-2000; 2000EP-0116126.
 XX
 PR 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isegaal T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX
 DR WPI, 2001-318749/34.
 XX
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX
 PS Claim 8; SEQ ID 19004; 2537PP + CD ROM; English.
 XX
 CC The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the

CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

XX
SQ Sequence 6060 BP; 1639 A; 1526 C; 1363 G; 1532 T; 0 other;

Query Match 96.0%; Score 2969.6; DB 22; Length 6060;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2994; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 96 CAACCTATACAAACAGATATCCGGTGTGCGCCCAAGCCGAGGAGGACACACACA 155
DB 1 CAACCTATACAAACAGATATCCGGTGTGCGCCCAAGCCGAGGAGGACACACACA 60

QY 156 GAGGACAGAGCTGAGATCCAGATGATATGATCATGAGAGGAAACCTCTACATGTGTC 215
DB 61 GAGGACAGAGCTGAGATCCAGATGATATGATCATGAGAGGAAACCTCTACATGTGTC 120

QY 216 TAGGAGACATATTTACTGTGATATAGACACATACACAGGAGGAAATTTATGTAG 275
DB 121 TAGGAGACATATTTACTGTGATATAGACACATACACAGGAGGAAATTTATGTAG 180

QY 276 CAAAAACATGATGGAATCTAGACAGCGCCGATGATGACATGACGAAATGAAAGGAAA 335
DB 181 CAAAAACATGATGGAATCTAGACAGCGCCGATGATGACATGACGAAATGAAAGGAAA 240

QY 336 ACATAGAGATGAGTGCACCAACTTATTAAGTCTCTTAAGAAAAACGATGATGAT 395
DB 241 ACATAGAGATGAGTGCACCAACTTATTAAGTCTCTTAAGAAAAACGATGATGAT 300

QY 396 GTTTGTGTGGAATATGCTTCAACCTCTCTGAGAAACTATAGATGATGAT 455
DB 301 GTTTGTGTGGAATATGCTTCAACCTCTCTGAGAAACTATAGATGATGATGAT 360

QY 456 GGAACCATGGGGGATTAATTCAGCGGATGGCCAGATGGCCATATGATGCAAAATGTC 515
DB 361 GGAACCATGGGGGATTAATTCAGCGGATGGCCAGATGGCCATATGATGCAAAATGTC 420

QY 516 CAAGCTTGCAGCTGTTTGCAGATGGAATACTAATCTAGCCACAGTGAATCTCTTGC 575
DB 421 CAAGCTTGCAGCTGTTTGCAGATGGAATACTAATCTAGCCACAGTGAATCTCTTGC 480

QY 576 CATGAGCAGATCTATTTACCGGAGTCTTGGAGAAAGCCCTAACCCTGGGACCGCAAGCA 635
DB 481 CATGAGCAGATCTATTTACCGGAGTCTTGGAGAAAGCCCTAACCCTGGGACCGCAAGCA 540

QY 636 CGATTCAAAATGGTTGAAGAACCACTTGTTCAGACCGGTGATATAGGAGATATAT 695
DB 541 CGATTCAAAATGGTTGAAGAACCACTTGTTCAGACCGGTGATATAGGAGATATAT 600

QY 696 CTACTCTTCTTCAAGGAATAGCAGTGGATATACACCATGGAAGAGTATGTTTCCC 755
DB 601 CTACTCTTCTTCAAGGAATAGCAGTGGATATACACCATGGAAGAGTATGTTTCCC 660

QY 756 AAGAGTGGTCAAGTTTGTAAAGATGATGATGGAGGATCAAGAGTCCGAGGAACA 815
DB 661 AAGAGTGGTCAAGTTTGTAAAGATGATGATGGAGGATCAAGAGTCCGAGGAACA 720

QY 816 GTGAGCTGCTCTCGAAGGCGCTTGAACCTGCTCAATCTCTGAGAGCTCTCAATTTTA 875

DB 721 GTGAGCTGCTCTCGAAGGCGCTTGAACCTGCTCAATCTCTGAGAGCTCTCAATTTTA 780

QY 876 TTTCACATTTCTCCAGGAGATTACAGATGATGATCTATACAGGCGGTGATGTGCT 935
DB 781 TTTCACATTTCTCCAGGAGATTACAGATGATGATCTATACAGGCGGTGATGTGCT 840

QY 936 GGCACAGTTTCTTACACCTTATATACAGATCCCTGGGTCTGACGTCTGTCCTATACAT 995
DB 841 GGCACAGTTTCTTACACCTTATATACAGATCCCTGGGTCTGACGTCTGTCCTATACAT 900

QY 996 GCTTGACATTTGCCAGTGTTTTCTGAGAGATTCAGGAACAGACAGTCTCTGATTCAC 1055
DB 901 GCTTGACATTTGCCAGTGTTTTCTGAGAGATTCAGGAACAGACAGTCTCTGATTCAC 960

QY 1056 CTGAGACACAGTTCCTGATGAGAGATTCCTTAAGCCAGGCGCAGTTGCTGCTGCTC 1115
DB 961 CTGAGACACAGTTCCTGATGAGAGATTCCTTAAGCCAGGCGCAGTTGCTGCTGCTC 1020

QY 1116 ATCCCTCTTGAAGAAATGATGCAACCTCCATGATGATGATGATGATGATGATGATGAT 1175
DB 1021 ATCCCTCTTGAAGAAATGATGCAACCTCCATGATGATGATGATGATGATGATGATGAT 1080

QY 1176 CAAGACGACCCGCTCATGATGAGGACAGTGCCTCCATCTCAACAGGCGCATGTCTCT 1235
DB 1081 CAAGACGACCCGCTCATGATGAGGACAGTGCCTCCATCTCAACAGGCGCATGTCTCT 1140

QY 1236 GAGAACATGTTGATACCGCTTACCAAAATTCAGTGGACACACACTGCTGGGCATA 1295
DB 1141 GAGAACATGTTGATACCGCTTACCAAAATTCAGTGGACACACACTGCTGGGCATA 1200

QY 1296 TCGAATACACAGTGTGTTTCTCGGATGAGAGAGGAGATCATCTGAGATTTTGGC 1355
DB 1201 TCGAATACACAGTGTGTTTCTCGGATGAGAGAGGAGATCATCTGAGATTTTGGC 1260

QY 1356 CAGAAATGAGAAATAGTGTGTTTCTAAATGACAGCTTTCTCTGAGAGAGATGAGTGT 1415
DB 1261 CAGAAATGAGAAATAGTGTGTTTCTAAATGACAGCTTTCTCTGAGAGAGATGAGTGT 1320

QY 1416 CAACCTCTG -AAAAATGACATATGATGAGTCCAGAACCAAAAGATATATGCGATGAGC 1474
DB 1321 CAACCTCTGAAAAATGACATATGATGAGTCCAGAACCAAAAGATATATGCGATGAGC 1380

QY 1475 TGGACAGAGAGAGCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1534
DB 1381 TGGACAGAGAGAGCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440

QY 1535 TTGGCCGCTGTGAACGACATGGGAAGT -AAAAAACTGTATTTGCTCCAGAGACCA 1593
DB 1441 TTGGCCGCTGTGAACGACATGGGAAGTAAAAAACTGTATTTGCTCCAGAGACCA 1500

QY 1594 TATTGTGATGATTAAGGAAGTGTGCTGCGACCAATTATACCCACAGAGACTG 1653
DB 1501 TATTGTGATGATTAAGGAAGTGTGCTGCGACCAATTATACCCACAGAGACTG 1560

QY 1654 ACTTTGAGCAGAGATAGAGCGTGGCAATACAGATGCTGGGGAGCTGTCACAATTC 1713
DB 1561 ACTTTGAGCAGAGATAGAGCGTGGCAATACAGATGCTGGGGAGCTGTCACAATTC 1620

QY 1714 TTTGTGCACTGAATGCGATCTCAATGCTCTTTCGCCAGCAACACCACTAGATTCG 1773
DB 1621 TTTGTGCACTGAATGCGATCTCAATGCTCTTTCGCCAGCAACACCACTAGATTCG 1680

QY 1774 ACGGCTCAAGGGGGTATGAGTCAAGGGAGAGATGCTGAGCTGGAAGCATCTGCTGAC 1833
DB 1681 ACGGCTCAAGGGGGTATGAGTCAAGGGAGAGATGCTGAGCTGGAAGCATCTGCTGAC 1740

QY 1834 TCACCTGACAGACAGACCCCTTTGGGGCACTGCTTCCCATATACCAAGACAAGAG 1893
DB 1741 TCACCTGACAGACAGACCCCTTTGGGGCACTGCTTCCCATATACCAAGACAAGAG 1800

QY 1894 GGAATGATGCGGAAAGTATCTAATAAGGCCAGACAGCTGTTCCGTAACCTCTG 1953

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Db      1801 GAGGTGATTCGGGAAGTACCTCAAGGCGACGACAGCTGGTTCCTCCGACCCCTCTTG 1860
QY      1954 GCCATTGACATCTCTGCTCTTCTGTCATGAGGGGCGCTCTCTGGGGCATACCGCTTAC 2013
      1861 GCCATTGACATCTCTGCTCTTCTGTCATGAGGGGCGCTCTCTGGGGCATACCGCTTAC 1920
QY      2014 TGGCTGTGATCATGAGGCGCAAGAGCGTGTGTGTGACGCGCAAGGGAAGGAGCTC 2073
      1921 TGGCTGTGATCATGAGGCGCAAGAGCGTGTGTGTGACGCGCAAGGGAAGGAGCTC 1980
Db      2074 ACCACTGCGGCGGGGCTCCATGACAGCGTCACCAAGCTCAGCGGCTCTTTGGGGAG 2133
      1981 ACCACTGCGGCGGGGCTCCATGAGAGCGTGTGTGTGACGCGCAAGGGAAGGAGCTC 2040
QY      2134 ACTCAATCCAAAGACCCAAAGCCGAGGCCATCTTACAGCCATCATGACAAAGCGCAAG 2193
      2041 ACTCAATCCAAAGACCCAAAGCCGAGGCCATCTTACAGCCATCATGACAAAGCGCAAG 2100
QY      2194 CTGCGCACTCCGCGCAACAGCGGCAAGATGCTCATTTAAAGCACTAGCACCACTTGGAC 2253
      2101 CTGCGCACTCCGCGCAACAGCGGCAAGATGCTCATTTAAAGCACTAGCACCACTTGGAC 2160
QY      2254 CTGACGCGCCCTCCCAACCCCAAGTCAACCCCAAGCTGACGAGAAAGCCAGC 2313
      2161 CTGACGCGCCCTCCCAACCCCAAGTCAACCCCAAGCTGACGAGAAAGCCAGC 2220
QY      2314 CCGGCGAGCCGCGAGTGGGAGAGGAACCAACCTCTCATGATGCTTGCAGAAAGGACATG 2373
      2221 CCGGCGAGCCGCGAGTGGGAGAGGAACCAACCTCTCATGATGCTTGCAGAAAGGACATG 2280
QY      2374 CCGGCGAGCCGCGAGTGGGAGAGGAACCAACCTCTCATGATGCTTGCAGAAAGGACATG 2433
      2281 CCGGCGAGCCGCGAGTGGGAGAGGAACCAACCTCTCATGATGCTTGCAGAAAGGACATG 2240
QY      2434 ATCCCAAGCTGTGTGTCTCTGCTCCATCAGCAGAGGCTTCCCAAGCATGATGATGATG 2493
      2341 ATCCCAAGCTGTGTGTCTCTGCTCCATCAGCAGAGGCTTCCCAAGCATGATGATGATG 2400
QY      2494 CAGGCCAAATGAGCGAGGTGGCCCATATGGCTGTGAGAGCAAGCGCGCGCACACTGGAG 2553
      2401 CAGGCCAAATGAGCGAGGTGGCCCATATGGCTGTGAGAGCAAGCGCGCGCACACTGGAG 2460
QY      2554 TATAGACATCAAGAGAACTCTCAGCAGCAAGAGTCCCAACCATGAGGGTGAACCTTGTG 2613
      2461 TATAGACATCAAGAGAACTCTCAGCAGCAAGAGTCCCAACCATGAGGGTGAACCTTGTG 2520
QY      2614 GAGAACTGACAGACCTTCCGCCCCCAAGTTCACAGGAGGAGGCTTCCCTGGGGCCCCCG 2673
      2521 GAGAACTGACAGACCTTCCGCCCCCAAGTTCACAGGAGGAGGCTTCCCTGGGGCCCCCG 2580
QY      2674 GAGAGCTGCTGTCTCAGACCGGTCTAAGCAAGCGGCTGGAAGTGAACCACTCTCTCC 2733
      2581 GAGAGCTGCTGTCTCAGACCGGTCTAAGCAAGCGGCTGGAAGTGAACCACTCTCTCC 2640
Db      2734 TACGGGGTTGACTTAAAGAGAGGTACCCACGAACTGCTCAGAGAGAACCCACAGGCC 2793
      2641 TACGGGGTTGACTTAAAGAGAGGTACCCACGAACTGCTCAGAGAGAACCCACAGGCC 2700
QY      2794 ACCACTTCAAAAAGAAACAACTAAGTCTTCAATTCCTCTCAGACCTTCCAGAAACAG 2853
      2701 ACCACTTCAAAAAGAAACAACTAAGTCTTCAATTCCTCTCAGACCTTCCAGAAACAG 2760
QY      2854 AGCTTTGAGAGGAGGAGCAACCCGCGCGCGCGCGCGAGAGGAGTGAATCTCAGAGTGTG 2913
      2761 AGCTTTGAGAGGAGGAGCAACCCGCGCGCGCGCGCGAGAGGAGTGAATCTCAGAGTGTG 2820
Db      2914 CACAGCTCCAGAGCTTCTGCGAGGCGCTGACTGTCTGAGGAGCAAGCCAGCTCAAGGCC 2973
      2821 CACAGCTCCAGAGCTTCTGCGAGGCGCTGACTGTCTGAGGAGCAAGCCAGCTCAAGGCC 2880
QY      2974 TACAACTCACTGACAGAGTGGGGGTGAAGGCTAGCCCTGCTTAAAGCCGAGAGCTATCC 3033
      2881 TACAACTCACTGACAGAGTGGGGGTGAAGGCTAGCCCTGCTTAAAGCCGAGAGCTATCC 2940

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QY      3034 CCCAACCAATCTTCTGCTCCCTTTCACATCCATGAGGCCAATGATGCTGTACATA 3093
      2941 CCCAACCAATCTTCTGCTCCCTTTCACATCCATGAGGCCAATGATGCTGTACATA 3000
Db
RESULT 5
AAV44295
ID AAV44295 standard; cDNA; 3550 BP.
AC AAV44295;
XX
XX 06-OCT-1998 (first entry)
DE Human secreted protein clone CJ145_1 cDNA.
XX
XX Secreted protein: human fetal brain; nutrition; cytokine; stimulant;
KW cell proliferation; differentiation; immune system; suppressor; ligand;
KW regulator; hematopoiesis; tissue growth; activin; inhibin; haemostatic;
KW chemotaxis; chemokinetic; thrombosis; receptor; cadherin; tumour;
KW anti-inflammatory; ds.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 126..3053
FT CDS /*tag= a
FT /*product= secreted protein
FT /note= "isolated from clone CJ145_1"
XX
XX W09827205-A2.
XX
XX 25-JUN-1998.
XX
XX 17-DEC-1997; 97WO-US23330.
XX
XX 16-DEC-1997; 97US-0991872.
XX 18-DEC-1996; 96US-0769192.
XX 13-JAN-1997; 97US-0783401.
XX
XX (GENE ) GENETICS INST INC.
XX
XX Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
PI Racle LA, Spaulding V, Treacy M;
XX
XX WPI: 1998-362774/31.
XX
XX P-PSDB: AAW64221.
XX
XX New polynucleotides and secreted proteins - obtained from human
XX foetal brain, human adult testes, human adult brain and human adult
XX salivary gland cDNA libraries
XX
XX P-PSDB: AAW64221.
XX
XX Claim 17a; Page 69-71; 110pp; English.
XX
XX This sequence encodes a novel secreted protein from clone CJ145_1
XX isolated from a human fetal brain cDNA library. This protein has
XX applications for nutritional use, cytokine and cell
XX proliferation/differentiation activity, immune stimulating or
XX suppressing activity, hematopoiesis regulating activity, tissue growth
XX activity, activin/inhibin activity, chemotactic/chemokinetic activity,
XX haemostatic and thrombotic activity, receptor/ligand activity,
XX anti-inflammatory activity, cadherin/tumour invasion suppressor activity,
XX tumour inhibitory activity and other activities.
XX
XX Sequence 3550 BP; 957 A; 994 C; 856 G; 742 T; 1 other;
SO
Query Match 88.8%; Score 2746.2; DB 19; Length 3550;
Best Local Similarity 94.5%; Pred. No. 0;
Matches 2923; Conservative 1; Mismatches 4; Indels 165; Gaps 1;
QY 1 ATGAGTGTGAGAGCCCTGCTGCTATATTTTCACTGCTACACTTTGCTGGGCTGTTTC 60
      126 ATGAGTGTGAGAGCCCTGCTGCTATATTTTCACTGCTACACTTTGCTGGGCTGTTTC 185

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QY	61	CCGAAAGATTTCGAGCCGACACGATTTTCGGATGGCAACTATACAAAACAGATCCGGG	120
Db	186	CCGAAAGATTCTAGCCAACTACATATTTCGATGGCACTATACAAAACAGATCCGGG	245
QY	121	TTTGTGGGCCACAGCCAGGACCGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG	180
Db	246	TTTGTGGGCCACAGCCAGGACCGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG	305
QY	181	ATTATGATCATGAAAGGAAACCCCTACATTGGCTGCTAGGGACCATTTATACCTGTGAT	240
Db	306	ATTATGATCATGAAAGGAAACCCCTACATTGGCTGCTAGGGACCATTTATACCTGTGAT	365
QY	241	ATTAGACATACACACACGAGAAGAAATTTATTGAGCAAAAAAATCTGACATGAAATCTAGA	300
Db	366	ATTAGACATACACACACGAGAAGAAATTTATTGAGCAAAAAAATCTGACATGAAATCTAGA	425
QY	301	CAGGCGGATGTAGACACATGACAGATGAAAGGAAAAACATAGAGTATGTCGCCACAATT	360
Db	426	CAGGCGGATGTAGACACATGACAGATGAAAGGAAAAACATAGAGTATGTCGCCACAATT	485
QY	361	ATTAAAGTCTCTTAAAGAAAAACGATGATGATTTGTGTGTGGAACTATAGCTTC	420
Db	486	ATTAAAGTCTCTTAAAGAAAAACGATGATGATTTGTGTGTGGAACTATAGCTTC	545
QY	421	AACCCCTCCGACGAAACCTATAGATGATGATATCTTGGAAACCATTTGGGGATGATTCACG	480
Db	546	AACCCCTCCGACGAAACCTATAGATGATGATATCTTGGAAACCATTTGGGGATGATTCACG	605
QY	481	GGAATGGCCGAGATGCCCATATGATGTCGCAAAACATGAGCCACGTTGCTGTTTCAGATGGA	540
Db	606	GGAATGGCCGAGATGCCCATATGATGTCGCAAAACATGAGCCACGTTGCTGTTTCAGATGGA	665
QY	541	AAACTATACACAGCAACAGTACTGATCTCTTGCCATTACCCAGTCAATTATCCGAGAT	600
Db	666	AAACTATACACAGCAACAGTACTGATCTCTTGCCATTACCCAGTCAATTATCCGAGAT	725
QY	601	CTTGAGAGAAACCCCTACCCCTGCGGACCCGTAAGACAGATTCAAAATGGTTGAAAGAACCA	660
Db	726	CTTGAGAGAAACCCCTACCCCTGCGGACCCGTAAGACAGATTCAAAATGGTTGAAAGAACCA	785
QY	661	TACTTTGTTCAGGCGGTGGATTAAGGAGATTAATCTCACTCTCTTCACAGGAAATAGCA	720
Db	786	TACTTTGTTCAGGCGGTGGATTAAGGAGATTAATCTCACTCTCTTCACAGGAAATAGCA	845
QY	721	GTGAGATATACACCATGGGAAAGGATGTTTCCCAAGAGTGGCTCAGGTTTGTAGAAAT	780
Db	846	GTGAGATATACACCATGGGAAAGGATGTTTCCCAAGAGTGGCTCAGGTTTGTAGAAAT	905
QY	781	GATATGGAGAGATCTCAAGAGTCCCTGGAGAAACAGTGGAGGTGCTCGAAGGCGCG	840
Db	906	GATATGGAGAGATCTCAAGAGTCCCTGGAGAAACAGTGGAGGTGCTCGAAGGCGCG	965
QY	841	TTGAACTGCTAGTTCCTGAGACTCTCATTTTATTTTCAACATTTCTCAGGCGATTACA	900
Db	966	TTGAACTGCTAGTTCCTGAGACTCTCATTTTATTTTCAACATTTCTCAGGCGATTACA	1025
QY	901	GATGATGATTCGATACAGGCGCGTGAATGTCTCTCGGCAACGTTTCTTACACCTATTAAC	960
Db	1026	GATGATGATTCGATACAGGCGCGTGAATGTCTCTCGGCAACGTTTCTTACACCTATTAAC	1085
QY	961	AGCATCCCTGGGTGCGAGTCTGTGSCATGACATGCTTGACATTTGGCAGTGTTTTACT	1020
Db	1086	AGCATCCCTGGGTGCGAGTCTGTGSCATGACATGCTTGACATTTGGCAGTGTTTTACT	1145
QY	1021	GGGAGATTCGAGAAACAGAACTCTCTGATTTCCACCTGAGACCAAGTTCTGATAGAACGA	1080
Db	1146	GGGAGATTCGAGAAACAGAACTCTCTGATTTCCACCTGAGACCAAGTTCTGATAGAACGA	1205
QY	1081	GTTCTTAAGCCAGGCGCGAGTTGCTGTGCTGGCTACATCTCCTTAGAAGAAATATGCAAC	1140
Db	1206	GTTCTTAAGCCAGGCGCGAGTTGCTGTGCTGGCTACATCTCCTTAGAAGAAATATGCAAC	1265

QY	1141	TCCAATGAGTTCCTCTATGATATACCCGGAACCTTCATCAAGAGCACCCGCTCATGGATAG	1200
Db	1266	TCCAATGAGTTCCTCTATGATATACCCGGAACCTTCATCAAGAGCACCCGCTCATGGATAG	1325
QY	1201	GCAGTGGCCCAATCTTCAACAGAGCCATGGTTCCTAGAAACATGGTGCAGTACCGCTT	1260
Db	1326	GCAGTGGCCCAATCTTCAACAGAGCCATGGTTCCTAGAAACATGGTGCAGTACCGCTT	1385
QY	1261	ACCAAAATTTGACGTGACACAGCTGCTGGGCCATATCAGAAATCACACTGTGTTTCTG	1320
Db	1386	ACCAAAATTTGACGTGACACAGCTGCTGGGCCATATCAGAAATCACACTGTGTTTCTG	1445
QY	1321	GGATCAGAGAAAGGAATCATCTTGAAGTTTTTGGCCAGAAATAGGAATATGTTGTTTCTA	1380
Db	1446	GGATCAGAGAAAGGAATCATCTTGAAGTTTTTGGCCAGAAATAGGAATATGTTGTTTCTA	1505
QY	1381	AATGACAGCCCTTTTCCGAGAGATAGAGTGTATACACTCTGTAATAAATAGCACTATGAT	1440
Db	1506	AATGACAGCCCTTTTCCGAGAGATAGAGTGTATACACTCTGTAATAAATAGCACTATGAT	1565
QY	1441	GGAGTCGAGACAAAAGATCATGGGCATGCAGCTGGAGACAGACAAAGCAAGCTCTGTAT	1500
Db	1566	GGAGTCGAGACAAAAGATCATGGGCATGCAGCTGGAGACAGACAAAGCAAGCTCTGTAT	1625
QY	1501	GTTCGCTTCTCTACTGTTGTATPAAGTTTCCCTTGTGCCGCTGTGAAGACATGGGAAG	1560
Db	1626	GTTCGCTTCTCTACTGTTGTATPAAGTTTCCCTTGTGCCGCTGTGAAGACATGGGAAG	1685
QY	1561	TGTAAAAAACCTGTATTTGCTCCAGAGACCCATTTGTGGATGGATTAAGAGAGTGTGT	1620
Db	1686	TGTAAAAAACCTGTATTTGCTCCAGAGACCCATTTGTGGATGGATTAAGAGAGTGTGT	1745
QY	1621	GCCTGCAAGCCATTATACCCCAACAGAGAGACTGACTTTTGAAGAGACATAGAGCGTGC	1680
Db	1746	GCCTGCAAGCCATTATACCCCAACAGAGAGACTGACTTTTGAAGAGACATAGAGCGTGC	1805
QY	1681	AATACAGATGTTCTGGGGAGCTGTCAACAATTCCTTGTGGCACTGAATGGGCATTCCAGT	1740
Db	1806	AATACAGATGTTCTGGGGAGCTGTCAACAATTCCTTGTGGCACTGAATGGGCATTCCAGT	1863
QY	1741	TCCCTCTTGCCCGACACACACATCAGATTCCAGCGGCTCAAGAGGGGTATGATGCTAGG	1800
Db	1864	-----	1863
QY	1801	GGAGAGATGCTGGAAGCTGGAGACATCTGCTTGACTCAGCTGACAGACAGACCTTTGGGG	1860
Db	1854	-----	1853
QY	1861	GCAGTGTCTTCCCAATATACCAAGACAGAAGGAGTGTGGGAAAGTTTACTCTCAAA	1920
Db	1854	-----	1880
QY	1921	GGCCACGACAGAGTGGTCCCGTCACCTTGTGGCAATTCAGATCAATCTGAGTTCGTGTC	1980
Db	1881	GGCCACGACAGAGTGGTCCCGTCACCTTGTGGCAATTCAGATCAATCTGAGTTCGTGTC	1940
QY	1981	ATGGGGGCGCTTCTCGGGCATCACGTTACTGCGTCTGTGTATCATTCGGCGCAAGAGAC	2040
Db	1941	ATGGGGGCGCTTCTCGGGCATCACGTTACTGCGCTGTGTGTATCATTCGGCGCAAGAGAC	2000
QY	2041	GTGGCTGTGTGTACAGCGTAAGGAGAAAGAGTCAACCACTGGCGCGGGGCTCCATAGC	2100
Db	2001	GTGGCTGTGTGTACAGCGTAAGGAGAAAGAGTCAACCACTGGCGCGGGGCTCCATAGC	2060
QY	2101	ATGCTGACCAACCTGAGCGGCTCTTTTGGGACACTCATCTCAAAAGAACCCAAAGCGGAG	2160
Db	2061	ATGCTGACCAACCTGAGCGGCTCTTTTGGGACACTCATCTCAAAAGAACCCAAAGCGGAG	2120
QY	2161	GGCATCTTCACCGCACTCATGCAACAAGGCAAGCTGCGCACTCCCGGACACAGGCCAAG	2220
Db	2121	GGCATCTTCACCGCACTCATGCAACAAGGCAAGCTGCGCACTCCCGGACACAGGCCAAG	2180
QY	2221	ATGCTCATTTAAAGGACAGACCAAGCAAGCTGGAATCTGAGGCGGCTGCCCAACCCAGAGTCA	2280

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Db      2181 ATGCTATTAAAGCAGACAGACACCACTGGACCTGACGGCCCTCCCAACCCAGAGTCA 2240
QY      2281 ACCCAAGCGCTGACAGACAGAGGAGAGCCCAAGCCCGGCGAGCGGAGTGGAGAGGAAAC 2340
Db      2241 ACCCAAGCGCTGACAGAGAGGAGAGCCCAAGCCCGGCGAGCGGAGTGGAGAGGAAAC 2300
QY      2341 CAGAACCTCATCAATACCTGACAGAAAGACATGCCCCCATGGGCTCCCTGTGATTCC 2400
Db      2301 CAGAACCTCATCAATACCTGACAGAAAGACATGCCCCCATGGGCTCCCTGTGATTCC 2360
QY      2401 ACGGACCTGCCCCCTGCGGCGCTCCCAAGCCACATCCCAAGCGTGTGCTCTCCCATC 2460
Db      2361 ACGGACCTGCCCCCTGCGGCGCTCCCAAGCCACATCCCAAGCGTGTGCTCTCCCATC 2420
QY      2461 ACGGACGAGGCTTACAGCATAGTACGTGAGACGCCCAAAATAGAGAGGAGGCGCGAG 2520
Db      2421 ACGGACGAGGCTTACAGCATAGTACGTGAGACGCCCAAAATAGAGAGGAGGCGCGAG 2480
QY      2521 ATGGGCGTGGAGAGACAGCGCCGACACAGTAGATATAGACCATCAAGAGACATCTCAGC 2580
Db      2481 ATGGGCGTGGAGAGACAGCGCCGACACAGTAGATATAGACCATCAAGAGACATCTCAGC 2540
QY      2581 ACGAAGATGCCAACCAGGAGGTGAACCTTTGGAGAGACCTTGACAGCGCTGCCCCCAAA 2640
Db      2541 ACGAAGATGCCAACCAGGAGGTGAACCTTTGGAGAGACCTTGACAGCGCTGCCCCCAAA 2600
QY      2641 GTTCCACAGCGGAGGCGCTCCCTGGGTGCCCGGAGGAGCCCTGCTCTAGACCGGTCTA 2700
Db      2601 GTTCCACAGCGGAGGCGCTCCCTGGGTGCCCGGAGGAGCCCTGCTCTAGACCGGTCTA 2660
QY      2701 AGCAAGCGGCTGGAAATGACACACACTCTCTTCTACGAGGAGGTGACTATAGAGAGACTAC 2760
Db      2661 AGCAAGCGGCTGGAAATGACACACACTCTCTTCTACGAGGAGGTGACTATAGAGAGACTAC 2720
QY      2761 CCCAGACACTCGCTCTCAGAGAGAGCCACACAGGCGCCACACTCTCTCTCTCTCTCTCTAC 2820
Db      2721 CCCAGACACTCGCTCTCAGAGAGAGCCACACAGGCGCCACACTCTCTCTCTCTCTCTCTAC 2780
QY      2821 TCTCCAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2880
Db      2781 TCTCCAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2840
QY      2881 CCGGCCCCCGAGAGGCTGAGCTCCATCCAGGTGACAGCTCCAGCCATCTGGCCAGGCC 2940
Db      2841 CCGGCCCCCGAGAGGCTGAGCTCCATCCAGGTGACAGCTCCAGCCATCTGGCCAGGCC 2900
QY      2941 GTGACTGTCTCGAGAGAGCCCGACGCTCAAGGCTTACACACTGACAGAGGTGGGGCTG 3000
Db      2901 GTGACTGTCTCGAGAGAGCCCGACGCTTCAAGGCTTACACACTGACAGAGGTGGGGCTG 2960
QY      3001 AAGGATGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3060
Db      2961 AAGGATGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3020
QY      3061 ACATCCATGAGAGCCCAATGATGCGTGTACATAA 3093
Db      3021 ACATCCATGAGAGCCCAATGATGCGTGTACATAA 3053

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RESULT 6
AAF98469
ID      AAF98469 standard; cdna; 3550 BP.
XX      AAF98469;
XX      07-JUN-2001 (first entry)
DE      Human cdna clone c0145_1 sequence seq ID 160.
XX      Human: secreted protein; nutrient; cytokine modulator; proliferation;
KW      differentiation; immune system modulator; tissue growth; chemotactic;
      haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; SS;

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KW      haematopoiesis.
XX      Homo sapiens.
OS      Homo sapiens.
XX      MO200119988-A1.
XX      22-MAR-2001.
XX      14-SEP-2000; 2000WO-DS25135.
XX      17-SEP-1999; 99US-0398829.
XX      (GENM) GENETICS INST INC.
XX      Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;
PI      Merberg D, Treacy M, Bowman MR, Spaulding V, Agostino MJ;
XX      MPI: 2001-244801/25.
XX      P-PSDB: AAB90731.
XX      Isolated nucleic acids encoding polypeptides, useful for modulating
PT      e.g. cytokine and cell proliferation/differentiation activity, the
PT      immune system and hematopoiesis regulating activity -
XX      Disclosure: Page 486-487; 557pp; English.
XX      Human cDNA clones represented in AAF98374 - AAF98489 encode secreted
XX      proteins AAB90667 - AAB90750. The cDNA clones are isolated from various
CC      tissue types, and may be used in the prevention, treatment and diagnosis
CC      of diseases associated with inappropriate protein expression. The
CC      polypeptides and nucleic acids may be used as nutrients or to modulate
CC      cytokine and cell proliferation/differentiation activity and may also be
CC      involved in modulation of the immune system. The cDNA sequences,
CC      proteins, their agonists and/or antagonists exhibit haematopoiesis
CC      regulating activity; tissue growth activity; activin/inhibin activity;
CC      chemotactic/chemokinetic activity; haemostatic and thrombolytic
CC      activity; receptor/ligand activity; anti-inflammatory activity; and/or
CC      haematopoiesis activity; cadherin/tumour suppressor activity; and/or
CC      tumour inhibition activity. Included in the invention are probes
CC      represented in AAF98490 - AAF98572 which are specific for the cDNA clones
CC      encoding the secreted proteins.
XX      Sequence 3550 BP; 957 A; 994 C; 856 G; 742 T; 1 other:
SQ
Query Match      88.8%; Score 2746.2; DB 22; Length 3550;
Best Local Similarity 94.5%; Pred. No. 0;
Matches 2923; Conservative 1; Mismatches 4; Indels 165; Gaps 1;
QY      1 ATGAGTCAAGAGCTTGTCTATATTTCACACTGCTACACTTGTGCGGCTGTTTC 60
Db      126 ATGAGTCAAGAGCTTGTCTATATTTCACACTGCTACACTTGTGCGGCTGTTTC 185
QY      61 CCAGAGATTTCTGAGCCATGATTTTTCGATGGCAACTTATCAAAAAGTATCGGCTG 120
Db      186 CCAGAGATTTCTGAGCCATGATTTTTCGATGGCAACTTATCAAAAAGTATCGGCTG 245
QY      121 TTTTGGGCCAAGAGCCAGAGAGCAACACAGAGGCGACAGGCTGAGCATCCAGATG 180
Db      246 TTTTGGGCCAAGAGCCAGAGAGCAACACAGAGGCGACAGGCTGAGCATCCAGATG 305
QY      181 ATTATGATCATGAGAGCAACCTCTACATTTGCTGTAGGACCATATTATCTGTTGAT 240
Db      306 ATTATGATCATGAGAGCAACCTCTACATTTGCTGTAGGACCATATTATCTGTTGAT 365
QY      241 ATAGACACATCACACAGGAGAAATTTATTGTAGCAAAAACAGTACATGGAATCTAGA 300
Db      366 ATAGACACATCACACAGGAGAAATTTATTGTAGCAAAAACAGTACATGGAATCTAGA 425
QY      301 CAGGCGGATGTAGACACATGCAAGATGAGGAGAAACATAGAGATGATGCGACAACTTT 360
Db      426 CAGGCGGATGTAGACACATGCAAGATGAGGAGAAACATAGAGATGATGCGACAACTTT 485
QY      361 ATTAAAGTCTTCTTAAGAAAAAGATGATGATTTGTTGCTGTGAGACTAATGCTTTC 420

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QY 2581 AGCAAGAGTCCCAACCATGGGGGTGAACCTTGTGAGAAACCTGAGACCTGCCCCCAAA 2640
 |||||
 DB 2541 AGCAAGAGTCCCAACCATGGGGGTGAACCTTGTGAGAAACCTGAGACCTGCCCCCAAA 2600
 |||||
 QY 2641 GTTCCACAGCGGGAGGCGCTCCCTGGGTCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA 2700
 |||||
 DB 2601 GTTCCACAGCGGGAGGCGCTCCCTGGGTCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA 2660
 |||||
 QY 2701 AGCAAGCGGCTGGAATGACACCTCTTCTTACGGGGTGTACTATTAAGAGAGCTAC 2760
 |||||
 DB 2661 AGCAAGCGGCTGGAATGACACCTCTTCTTACGGGGTGTACTATTAAGAGAGCTAC 2720
 |||||
 QY 2761 CCACAGACTCGCTCAGAGAAACCAACGAGGACACCTCACTCAAAAAGAAACAACTAAC 2820
 |||||
 DB 2721 CCACAGACTCGCTCAGAGAAACCAACGAGGACACCTCACTCAAAAAGAAACAACTAAC 2780
 |||||
 QY 2821 TCCCTCAATTCCTCTCACCCTCTCCAGAAACCAAGAGCTTGGCAGGGAGACAAACCGCGC 2880
 |||||
 DB 2781 TCCCTCAATTCCTCTCACCCTCTCCAGAAACCAAGAGCTTGGCAGGGAGACAAACCGCGC 2840
 |||||
 QY 2881 CCGGCGCCGAGAGGGTGAATCTCATCTCCAGGTGACAGAGCTCCAGGCACTGTGGCCAGGCG 2940
 |||||
 DB 2841 CCGGCGCCGAGAGGGTGAATCTCATCTCCAGGTGACAGAGCTCCAGGCACTGTGGCCAGGCG 2900
 |||||
 QY 2941 GTGACTGTCTCGAGGAGCCCAAGCCTCAACGCTTACACTGACAAAGTGGGGGCTG 3000
 |||||
 DB 2901 GTGACTGTCTCGAGGAGCCCAAGCCTTACACTGACAAAGTGGGGGCTG 2960
 |||||
 QY 3001 AAGCGTAGCGCCCTCGCTTAAAGCCGAGGTAACCCCAAAACATCTCTTCCCTTTC 3060
 |||||
 DB 2961 AAGCGTAGCGCCCTCGCTTAAAGCCGAGGTAACCCCAAAACATCTCTTCCCTTTC 3020
 |||||
 QY 3061 ACATTCATGAAGCCCAATGATGGGTACTATA 3093
 |||||
 DB 3021 ACATTCATGAAGCCCAATGATGGGTACTATA 3053
 |||||

RESULT 7
 ID AAA93618 standard; DNA; 3333 BP.
 XX
 AC AAA93618;
 XX
 DF 16-JAN-2001 (first entry)
 XX
 DE human semaphorin protein-like splice variant SECX 2864933-2 DNA.
 XX
 KW SECX protein; human; secreted; membrane-associated; cancer;
 KW proliferation regulator; differentiation regulator; non-malignant tumour;
 KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
 KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
 KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
 KW neurological disease; Alzheimer's disease; trauma; wounding;
 KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;
 KW anti-HIV; antiinflammatory; antiarthritic; antiatherosclerotic;
 KW neuroprotective; vulnary; antiallergic; antimicrobial; cardiant;
 KW dermatological; gene therapy; ds.
 KW
 OS Homo sapiens.
 XX
 PN MO200053742-A2.
 XX
 ED 14-SEP-2000.
 XX
 PF 09-MAR-2000; 2000WO-US06280.
 XX
 PR 09-MAR-1999; 99US-0123667.
 XX
 PR 08-MAR-2000; 2000US-0123667.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA;

XX
 DR WPI: 2000-594318/56.
 DR P-FSDB; AAB23031.
 XX
 PT Novel human membrane associated or secreted polypeptides and
 PT polynucleotides useful for diagnosis, prevention and treatment of
 PT pathological states such as cancer, immune, cardiovascular and
 PT neurological disorders
 XX
 PS Claim 3; Fig 3; 151pp: English.
 XX
 CC Sequences AAA93618-A93631 and AAA93673-A93676 represent nucleic acids
 CC which encode human SECX proteins (AAB23029-B23048). The SECX proteins
 CC of the invention are either secreted or membrane-associated proteins
 CC and act as regulator of cellular proliferation and differentiation. SECX
 CC proteins or nucleotides are useful for diagnosing the presence of, or
 CC predisposition to, a disease associated with altered levels of SECX
 CC proteins and nucleotides. The SECX proteins are also useful to screen
 CC compounds that modulate SECX activity or expression. The interaction of
 CC a SECX protein with other cellular proteins may be useful to modulate
 CC the activity of a partner protein, cellular proliferation, cellular
 CC differentiation and cell survival. SECX nucleotides are useful for the
 CC recombinant expression of SECX protein, and may be used to detect SECX mRNA
 CC or genetic lesions in the SECX gene. They may also be used to modulate
 CC SECX expression (e.g., using antisense oligonucleotides). SECX nucleic
 CC acid sequences are also useful for identifying a cell or tissue type in
 CC a biological sample, and in forensic biology. SECX primers or probes are
 CC useful for detecting the presence of SECX nucleotides and for screening
 CC tissue cultures for contamination. Diseases that may be treated or
 CC prevented using SECX proteins or nucleotides include cancer (e.g.,
 CC colorectal carcinoma, prostate cancer), benign tumours, immune disorders
 CC (including autoimmune diseases, transplant rejection, allergies, AIDS),
 CC infections, inflammatory disorders, arthritis, haematopoietic disorders,
 CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,
 CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g.,
 CC surgical or traumatic wounds, spinal cord injury), and skeletal
 CC disorders.
 CC
 XX
 SQ Sequence 3333 BP; 874 A; 921 C; 845 G; 692 T; 1 other;
 Query Match 87.2%; Score 2698; DB 21; Length 3333;
 Best Local Similarity 93.9%; Pred. No. 0;
 Matches 2907; Conservative 0; Mismatches 21; Indels 167; Gaps 3;
 QY 1 ATGAGTCTCAGAAAGCCTTGTCTATATTTACACTGCTACACTTGTCTGGGCTGTTTC 60
 |||||
 DB 214 ATGAGTCTCAGAAAGCCTTGTCTATATTTACACTGCTACACTTGTCTGGGCTGTTTC 273
 |||||
 QY 61 CCAGAAATTTCTGAGCCCAATTCATTTCTGATGGCACTATACAAACAGTATCCGGTG 120
 |||||
 DB 274 CCAGAAATTTCTGAGCCCAATTCATTTCTGATGGCACTATACAAACAGTATCCGGTG 333
 |||||
 QY 121 TTGTGGGCCCAGAGCCAGAGGAGCAACACACAGAGGCGACAGCTGGACATCCAGATG 180
 |||||
 DB 334 TTGTGGGCCCAGAGCCAGAGGAGCAACACACAGAGGCGACAGCTGGACATCCAGATG 393
 |||||
 QY 181 ATATGATCATGAACGGAACCTCTACATCTGCTGTAGGACCATATTTATACGTGAT 240
 |||||
 DB 394 ATATGATCATGAACGGAACCTCTACATCTGCTGTAGGACCATATTTATACGTGAT 453
 |||||
 QY 241 ATAGACATCATCAGACAGGAGAAATTTATTTGTAGCAAAAACAGTACATGAAATCTGA 300
 |||||
 DB 454 ATAGACATCATCAGACAGGAGAAATTTATTTGTAGCAAAAACAGTACATGAAATCTGA 513
 |||||
 QY 301 CAGGCGCATGTAGACATGACATGAGATGAAGGAAAAATTAAGATGAGTGCACACACTT 360
 |||||
 DB 514 CAGGCGCATGTAGACATGACATGAGATGAAGGAAAAATTAAGATGAGTGCACACACTT 573
 |||||
 QY 361 ATTAAGTCTTCTTAAGAAAAAGATATGATGTTGTGCTGGAAGTAAGGCTTC 420
 |||||
 DB 574 ATTAAGTCTTCTTAAGAAAAAGATATGATGTTGTGCTGGAAGTAAGGCTTC 633
 |||||
 QY 421 AACCTTCTCGAGAAACTATAGATGATGATGATGAAACCATTCGGGGATGAAATGAGC 480

Db 634 AACCCCTCCGAGAACTATAGATGATACATTGGAACCATTCGGGGATTAATTCAGC 693
 QY 481 GGAATGGCCAGATGGCCATATGATGCAACATGCAACGTGCACTGTTGCAGATGGA 540
 Db 694 GGAATGGCCAGATGGCCATATGATGCAACATGCAACGTGCACTGTTGCAGATGGA 753
 QY 541 AACTATATCTAGCCACAGTGAATGATCTCTGCAATGAGCAGTCAATTTACCGAGT 600
 Db 754 AACTATATCTAGCCACAGTGAATGATCTCTGCAATGAGCAGTCAATTTACCGAGT 813
 QY 601 CTTGGAGAAAGCCCTTACCTGCGACCGTCAAGCAGATTCAAATGTTGAAAGAACCA 660
 Db 814 CTTGGAGAAAGCCCTTACCTGCGACCGTCAAGCAGATTCAAATGTTGAAAGAACCA 873
 QY 661 TACTTTGTTCAAGCCGTGATTAAGAGATATATCTACTCTCTTCGAGAAATAGCA 720
 Db 874 TACTTTGTTCAAGCCGTGATTAAGAGATATATCTACTCTCTTCGAGAAATAGCA 933
 QY 721 GTGAGATATACACCATGAGGAAAGTAGTTTCCCAAGAGTGGCTCAGTTTGAAGAT 780
 Db 934 GTGAGATATACACCATGAGGAAAGTAGTTTCCCAAGAGTGGCTCAGTTTGAAGAT 993
 QY 781 GATATGGAGAGATCTCAAGAGTCTCGAGAAACAGTGGACGTGCTCGAGAGGCGCG 840
 Db 994 GATATGGAGAGATCTCAAGAGTCTCGAGAAACAGTGGACGTGCTCGAGAGGCGCG 1053
 QY 841 TTGAATGCTCAGTTCTCGAGAGTCTCAATTTTATTTCAAGATTCGACAGGAGTTACA 900
 Db 1054 TTGAATGCTCAGTTCTCGAGAGTCTCAATTTTATTTCAAGATTCGACAGGAGTTACA 1113
 QY 901 GATGATATGATATCAACGGCGGTGATGTTGCTCGGCAAGTTTCTACCTTTATAC 960
 Db 1114 GATGATATGATATCAACGGCGGTGATGTTGCTCGGCAAGTTTCTACCTTTATAC 1173
 QY 961 AGCATCCCTGGGTCTGACGTGCTGCTATGACATCTTGACATTCGACAGTGGTTTACT 1020
 Db 1174 AGCATCCCTGGGTCTGACGTGCTGCTATGACATTCGACATTCGACAGTGGTTTACT 1233
 QY 1021 GGGAGATTCAGAGACAGAGTCTGATTCACCTGAGACACAGTTCCTGATGAGACA 1080
 Db 1234 GGGAGATTCAGAGACAGAGTCTGATTCACCTGAGACACAGTTCCTGATGAGACA 1293
 QY 1081 GTTCTCAAGCCGAGGCGAGTGTGCTGCTGCTGCTCAATCTCTTAAGAAATATGCAAC 1140
 Db 1294 GTTCTCAAGCCGAGGCGAGTGTGCTGCTGCTGCTCAATCTCTTAAGAAATATGCAAC 1353
 QY 1141 TCCAAATGATTCCTGATGATACCTGATCACTATCAGACGACCCGCTCATGATGAG 1200
 Db 1354 TCCAAATGATTCCTGATGATACCTGATCACTATCAGACGACCCGCTCATGATGAG 1413
 QY 1201 GCAATGCCCTCCATCTTCAACAGGCGCATGTTCTCTGAGAACATGTCAGATACCGCTT 1260
 Db 1414 GCAATGCCCTCCATCTTCAACAGGCGCATGTTCTCTGAGAACATGTCAGATACCGCTT 1473
 QY 1261 ACCAAATGTCAGTGGACACAGTGTGCTGGGCGCAATAGAAATCACTGTGGTTTCTG 1320
 Db 1474 ACCAAATGTCAGTGGACACAGTGTGCTGGGCGCAATAGAAATCACTGTGGTTTCTG 1533
 QY 1321 GGATCAGAGAGGAATCATCTTGAAGTTTGGCCAGATAGGAATAGTGTGTTCTA 1380
 Db 1534 GGATCAGAGAGGAATCATCTTGAAGTTTGGCCAGATAGGAATAGTGTGTTCTA 1593
 QY 1381 AATGACAGCCCTTTTCTGAGAGAGATAGTGTTTACAACCTCTGAAAAATGACGTATGAT 1440
 Db 1594 AATGACAGCCCTTTTCTGAGAGAGATAGTGTTTACAACCTCTGAAAAATGACGTATGAT 1653
 QY 1441 GGAGTGCAGACAAAGAGATCATGGGCATGAGTGGACAGAGAGAGAGAGTCTCTGAT 1500
 Db 1654 GGAGTGCAGACAAAGAGATCATGGGCATGAGTGGACAGAGAGAGAGTCTCTGAT 1713
 QY 1501 GTTCGTTCTTACTCTGTGTGATTAAGTTCCCTTGGCCGCTGTAACGACATGGGAG 1560

Db 1714 GTTCGTTCTTACTGTGTGATTAAGTTCCCTTGGCCGCTGTGAAGACATGGGAG 1773
 QY 1561 TGTAAAAAACCTGTATTTGCTCCAGAGACCCATATGATGATGATTAAGAGAGTGT 1620
 Db 1774 TGTAAAAAACCTGTATTTGCTCCAGAGACCCATATGATGATGATTAAGAGAGTGT 1833
 QY 1621 GCCTGACGATTTTATCACCCAGACAGACATCTTTGACACAGATAGAGGTGAC 1680
 Db 1834 GCCTGACGATTTTATCACCCAGACAGACATCTTTGACACAGATAGAGGTGAC 1893
 QY 1681 AATACAGATGCTGGGGGAGCTGTCAATTCCTTTGGGCACTGATAGGCAATTCAGT 1740
 Db 1894 AATACAGATGCTGGGGGAGCTGTCAATTCCTTTGGGCACTGATAGGCAATTCAGT 1941
 QY 1741 TCCCTTTGGCCAGACAAACCATTCAGATTCGAGGCTCAAGAGGGGATATAGTATAG 1800
 Db 1942 ----- 1941
 QY 1801 GAGAGATGCTGGAGTGAAGATCTGTTGACTACAGACAGACACCTTTGGGG 1860
 Db 1942 ----- 1941
 QY 1861 GCAGTCTCTCCATATATCAACAGACAAAGGAGTATTCGGGAAAGTTTACTCATA 1920
 Db 1942 ----- 1941
 QY 1921 GGCACAGACAGGTGTTCCCGTACCTCTTGGGCACTGATGATCTGCTGCTTCTGTC 1980
 Db 1969 GGCACAGACAGGTGTTCCCGTACCTCTTGGGCACTGATGATCTGCTGCTTCTGTC 2028
 QY 1981 ATGGGGGCGGTCTTCTGAGGAGATCACCGTCTACTGCTGTGATCATGCGGCGCAAGAC 2040
 Db 2029 ATGGGGGCGGTCTTCTGAGGAGATCACCGTCTACTGCTGTGATCATGCGGCGCAAGAC 2088
 QY 2041 GTGGCTGTGTGAGCGCAAGAGAGAGTCAACCACTGCGCGGGGCTCCATGAGAC 2100
 Db 2089 GTGGCTGTGTGAGCGCAAGAGAGAGTCAACCACTGCGCGGGGCTCCATGAGAC 2148
 QY 2101 AGGTCACCAAGCTCAAGCGGCTCTTTGGGAGACTCAATCCAAAGCCCAAGCCGAG 2160
 Db 2149 AGGTCACCAAGCTCAAGCGGCTCTTTGGGAGACTCAATCCAAAGCCCAAGCCGAG 2208
 QY 2161 GCCATCTCAAGCGCTATGACCAACAGGAGTGGCTGCGCTCCCGCAACAGGCTCAAG 2220
 Db 2209 GCCATCTCAAGCGCTATGACCAACAGGAGTGGCTGCGCTCCCGCAACAGGCTCAAG 2268
 QY 2221 ATGCTCATTAAGCAGAGCCAGACCACTGAGCTGAGGCGCTCCCGCAACAGGCTCA 2280
 Db 2269 ATGCTCATTAAGCAGAGCCAGACCACTGAGCTGAGGCGCTCCCGCAACAGGCTCA 2328
 QY 2281 ACCCAACGCTGACAGCAGAGCCAGACCGGCGGACCGCGGAGTGGGAGAGAGAAC 2340
 Db 2329 ACCCAACGCTGACAGCAGAGCCAGACCGGCGGAGCGGCGGAGTGGGAGAGAGAAC 2388
 QY 2341 CAGAACTCATCAATGCTGTGACAAAGAGATGCCCCCATGGGCTCCCTGTGATTCGC 2400
 Db 2389 CAGAACTCATCAATGCTGTGACAAAGAGATGCCCCCATGGGCTCCCTGTGATTCGC 2448
 QY 2401 ACGGACCTGCCCCGCGGGGCTCCCGAGCCATCCCAAGCGGTGTGCTGCCCCATC 2460
 Db 2449 ACGGACCTGCCCCGCGGGGCTCCCGAGCCATCCCAAGCGGTGTGCTGCCCCATC 2508
 QY 2461 ACGGACGAGGCTTACAGCATGATGATGAGCCAGCCCAAAATGAGCGAGTGGCCAG 2520
 Db 2509 ACGGACGAGGCTTACAGCATGATGATGAGCCAGCCCAAAATGAGCGAGTGGCCAG 2568
 QY 2521 ATGGCGCTGAGAGACAGGCGGACACACTGAGATTAAGACCATCAAGAGACATCTAGC 2580
 Db 2569 ATGGCGCTGAGAGACAGGCGGACACACTGAGATTAAGACCATCAAGAGACATCTAGC 2628
 QY 2581 AGCAAGATGCCAATCATGAGGTGACCTTGTGAGAACTGAGACAGCTGCCCCCAAA 2640
 Db 2629 AGCAAGATGCCAATCATGAGGTGACCTTGTGAGAACTGAGACAGCTGCCCCCAAA 2688

QY 2641 GTTTCACAGGGGAGGCTCCCTGGGTGCTCCCGGGAGCTCCCTGTCAGACCGGTCTA 2700
 |||||||
 Db 2689 GTTTCACAGGGGAGGCTCCCTGGGTGCTCCCGGGAGCTCCCTGTCAGACCGGTCTA 2748
 |||||||
 QY 2701 ACACAGGCTGCTGAAATGACACCACTCTCTTCTACGGGGTGTGACTATTAAGAGGAGCTAC 2760
 |||||||
 Db 2749 ACACAGGCTGCTGAAATGACACCACTCTCTTCTACGGGGTGTGACTATTAAGAGGAGCTAC 2808
 |||||||
 QY 2761 CCACAGACTGCTCTACGAGAACCCACAGGCGACC-ACCTCTCAAAAGAAACACTTA 2819
 |||||||
 Db 2809 CCACAGACTGCTCTACGAGAACCCACAGGCGACC-ACCTCTCAAAAGAAACACTTA 2868
 |||||||
 QY 2820 CTCCTCAATCTCTCTC-ACCTCTCAAGAAACCAAGAGCTTTGGCAGGGAGAACCCCGC 2878
 |||||||
 Db 2869 CCGCCGCAATTCACMCTCTCTCTCAAAAGGAGACAGAGCTTTGGCAGGGAGAACCCCGC 2928
 |||||||
 QY 2879 CCGCCGCGCCGAGAGGGGTGAGACTCCATCCAGGTGACAGACTCCAGCCATCTGGCCAG 2938
 |||||||
 Db 2929 CCGCCGCGCCGAGAGGGGTGAGACTCCATCCAGGTGACAGACTCCAGCCATCTGGCCAG 2988
 |||||||
 QY 2939 CCGTGAAGTCTCTGAGGAGACCCAGCCTCAACGCTCAACTCACTGACAGAGTGGGGC 2998
 |||||||
 Db 2989 CCGTGAAGTCTCTGAGGAGACCCAGCCTCAACGCTCAACTCACTGACAGAGTGGGGC 3048
 |||||||
 QY 2999 TGAAGGCTAGCGCCCTGGCTAAAGCCGAGAGTACCCCGCAAGCATCTTGTCCCTTT 3058
 |||||||
 Db 3049 TGAAGGCTAGCGCCCTGGCTAAAGCCGAGAGTACCCCGCAAGCATCTTGTCCCTTT 3108
 |||||||
 QY 3059 CCACATCATGAGCCCAATGATGCTGATCATTA 3093
 |||||||
 Db 3109 CCACATCATGAGCCCAATGATGCTGATCATTA 3143
 |||||||

RESULT 8
 AAS68807
 ID AAS68807 standard; cDNA; 3039 BP.
 XX
 AC AAS68807;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #4611.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI: 2001-639362/73.
 DR P-PSDB: ABG04620.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 1; SEQ ID No 4611, 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WPIO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX

SQ Sequence 3039 BP; 741 A; 869 C; 781 G; 648 T; 0 other;

Query Match 71.8%; Score 2221.8; DB 23; Length 3039;

Best local Similarity 91.2%; Pred. No. 0; Mismatches 167; Indels 66; Gaps 2;

Matches 2408; Conservative 0;

QY 519 CGTTGACATGTTGACATGGAAGAAACATATCTAGCCAGCAGTCACTCTCTTCCAT 578
 |||||||
 Db 399 CTGACTCTCTCTTCACATGGAAGAAACATATCTAGCCAGCAGTCACTCTCTTCCAT 458
 |||||||
 QY 579 TGAAGCAGTATTTACCGGAGCTTTGAGAAAGCCCTACCTCGGACCGTCAAGCAGA 638
 |||||||
 Db 459 TGAAGCAGTATTTACCGGAGCTTTGAGAAAGCCCTACCTCGGACCGTCAAGCAGA 518
 |||||||
 QY 639 TTCAAAATGTTGAAGAAACATATCTTTGTCACAGCGGTGATTAAGAGATTTATCTA 698
 |||||||
 Db 519 TTCAAAATGTTGAAGAAACATATCTTTGTCACAGCGGTGATTAAGAGATTTATCTA 578
 |||||||
 QY 699 CTCTCTCTGAGAAATAGCAGTATTAACCATGGAAGGATGTTTCCCAAG 758
 |||||||
 Db 579 CTCTCTCTGAGAAATAGCAGTATTAACCATGGAAGGATGTTTCCCAAG 638
 |||||||
 QY 759 AGTGGCTCAGTTTGTAAAGATGATATGAGGAGATCTCAAGAGCTCGGAGAAACAGTG 818
 |||||||
 Db 639 AGTGGCTCAGTTTGTAAAGATGATATGAGGAGATCTCAAGAGCTCGGAGAAACAGTG 698
 |||||||
 QY 819 GAGGTCGTTCTGAAAGGCGCTGAACTGCTCAGTCTCAGAGCTCTCAATTTTATTT 878
 |||||||
 Db 699 GAGGTCGTTCTGAAAGGCGCTGAACTGCTCAGTCTCAGAGCTCTCAATTTTATTT 758
 |||||||
 QY 879 CAACATTCAGGAGGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 938
 |||||||
 Db 759 CAACATTCAGGAGGATTAAGATGATGATGATGATGATGATGATGATGATGATGATG 818
 |||||||
 QY 939 AACGTTTCTACACCTTTATACAGATCCCTGGGCTCAGCTGTGCTATGACATGCT 998
 |||||||
 Db 819 AACGTTTCTACACCTTTATACAGATCCCTGGGCTCAGCTGTGCTATGACATGCT 878
 |||||||
 QY 999 TGACATTCGACAGTGTGTTTACGAGATTCAGAGAAAGAGTCTCTGATTCACACTG 1058
 |||||||
 Db 879 TGACATTCGACAGTGTGTTTACGAGATTCAGAGAAAGAGTCTCTGATTCACACTG 938
 |||||||
 QY 1059 GACACCACTTCTGATGAAGAGTCTTAAGCCGAGGCTGCTGCTGCTGCTGCTGCTGCT 1118
 |||||||
 Db 939 GACACCACTTCTGATGAAGAGTCTTAAGCCGAGGCTGCTGCTGCTGCTGCTGCTGCT 998
 |||||||
 QY 1119 CTCCTTAAGAAATATGACAGCTCAAGTATGCTGATGATGATGATGATGATGATGATG 1178
 |||||||
 Db 999 CTCCTTAAGAAATATGACAGCTCAAGTATGCTGATGATGATGATGATGATGATGATG 1058
 |||||||
 QY 1179 GACGACCGCTCATGATGAGGAGTGGCTTCATCTTCAACAGGCGATGCTCTGAG 1238
 |||||||

Db 1059 GAGCAGCCCGCTCATGATGAGGAGGAGTGCCTCCATCTTCAACAGGCCATGGTTCCTGAG 1118
 QY 1239 AACATGGTGCATATCCCGCTTACCAAAATGSCATGAGACAGTGCCTGGGSCATATCA 1298
 Db 1119 AACAAATGGCATATCCCGCTTACCAAAATGSCATGAGACAGTGCCTGGGSCATATCA 1178
 QY 1299 GATACACACTGTGTGTTTCTGAGATCAGAGAGGAAATCATCTTGAAGTTTTCGCGAG 1358
 Db 1179 GATACACACTGTGTGTTTCTGAGATCAGAGAGGAAATCATCTTGAAGTTTTCGCGAG 1238
 QY 1359 AATGAGAAATAGTGTGTTTCTTAATGACAGCTTTTCCGAGAGATGAGTGTATACAA 1418
 Db 1239 AATGAGAAATAGTGTGTTTCTTAATGACAGCTTTTCCGAGAGATGAGTGTATACAA 1298
 QY 1419 CTTGTAATAATGATGATGATGAGTGAAGTGAACAAAAGATCATGAGGATGAGTGTGGA 1478
 Db 1299 CTTGTAATAATGATGATGATGAGTGAAGTGAACAAAAGATCATGAGGATGAGTGTGGA 1358
 QY 1479 CAGAGCAAGCAGCTCTGTATATGTTGCGTTCTCTACCTGTGTATGATTAAGTTCCTTGG 1538
 Db 1359 CAGAGCAAGCAGCTCTGTATATGTTGCGTTCTCTACCTGTGTATGATTAAGTTCCTTGG 1418
 QY 1539 CCGGTGTGACACATGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1598
 Db 1419 CCGGTGTGACACATGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1478
 QY 1599 TGGATGATTAAGAGAGTGTGTCCTGACAGCATTATCATCCCAACAGCAG-----ACTG 1653
 Db 1479 TGGATGATTAAGAGAGTGTGTCCTGACAGCATTATCATCCCAACAGCAG-----ACTG 1538
 QY 1479 TGGATGATTAAGAGAGTGTGTCCTGACAGCATTATCATCCCAACAGCAG-----ACTG 1538
 Db 1539 TGGATGATTAAGAGAGTGTGTCCTGACAGCATTATCATCCCAACAGCAG-----ACTG 1478
 QY 1654 ACTTTGACAGCAGCATTATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1713
 Db 1539 AGGCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1598
 QY 1714 TTGTGCGACTGATGAGGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1773
 Db 1599 ACTATGAGAGCAGCAGCAGTCCATCATCATCATCATCATCATCATCATCATCATCATCAT 1658
 QY 1774 AGGCTTCAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1794
 Db 1659 AGGCTTCAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1718
 QY 1795 -----TCTAGGGAGAGATGCTGACTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1832
 Db 1719 GTCTTACAGCTTAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1778
 QY 1833 CTACCTGAGAGCAGCAGCAGTTCGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1892
 Db 1779 CAGAGCAGAGGCTCCGTTGAGCAGCAGCAGTTCGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1838
 QY 1893 GGGAGTATGAGGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1952
 Db 1839 GAGAGTATGAGGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1898
 QY 1953 GGGCATTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2012
 Db 1899 GGGCATTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1958
 QY 2013 CTGCGTGTGATCATGAGGAGCAGCAGTTCGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2072
 Db 1959 CTGCGTGTGATCATGAGGAGCAGCAGTTCGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2018
 QY 2073 CAGCAGCTGAGCAGCAGCAGTTCGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2132
 Db 2019 CAGCAGCTGAGCAGCAGCAGTTCGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2078
 QY 2133 CACTCAATCCAAAGACCCAAAGCCGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2192
 Db 2079 CACTCAATCCAAAGACCCAAAGCCGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2138
 QY 2193 GCTGCGCAGTCCGAGCAGCAGCAGTTCGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2252
 Db 2139 GCTGCGCAGTCCGAGCAGCAGCAGTTCGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2198

QY 2253 CTTGAGGAGCCTTCCCGCAGAGTCAACCCCAAGCTGAGCAGAGAGGAGAGCAGCAG 2312
 Db 2199 CTTGAGGAGCCTTCCCGCAGAGTCAACCCCAAGCTGAGCAGAGAGGAGAGCAGCAG 2258
 QY 2313 CCGGCGCAGCAGCAGTGAAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2372
 Db 2259 CCGGCGCAGCAGCAGTGAAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2318
 QY 2373 GCGCCCGCATGGGCTCCCGTGTATTCACAGAGCAGTGCCTGCGGAGGCTCCCGCAGCAG 2432
 Db 2319 GCGCCCGCATGGGCTCCCGTGTATTCACAGAGCAGTGCCTGCGGAGGCTCCCGCAGCAG 2378
 QY 2433 CATCCCGAGCAGTGTGTTCTCCATCAGCAGCAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2492
 Db 2379 CATCCCGAGCAGTGTGTTCTCCATCAGCAGCAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2438
 QY 2493 CCAGCCCGCAATGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2552
 Db 2439 CCAGCCCGCAATGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2498
 QY 2553 GTATAAGACCATCAAGAGATCTGAGCAGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2612
 Db 2499 GTATAAGACCATCAAGAGATCTGAGCAGCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2558
 QY 2613 GAGAGACCTGAGACAGCTGCGCCCGCAAGTTCACAGCAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2672
 Db 2559 GAGAGACCTGAGACAGCTGCGCCCGCAAGTTCACAGCAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2618
 QY 2673 GGGAGCCTCCCTGCTCAAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2732
 Db 2619 GGGAGCCTCCCTGCTCAAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2678
 QY 2733 CTACGAGGTTGACTATAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2792
 Db 2679 CTACGAGGTTGACTATAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2738
 QY 2793 CACCACTCTCAAAAGAAACACACTAATCTCTCAATCTCTCAATCTCTCAATCTCTCAATCTCTCAATCTCTCAATCTCTCA 2852
 Db 2739 CACCACTCTCAAAAGAAACACACTAATCTCTCAATCTCTCAATCTCTCAATCTCTCAATCTCTCAATCTCTCAATCTCTCA 2798
 QY 2853 GAGCTTTGGCAGGAGGAGACACCCCGCGCCCGCAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2912
 Db 2799 GAGCTTTGGCAGGAGGAGACACCCCGCGCCCGCAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2858
 QY 2913 GCAAGAGTCCAGCAGCAGTTCGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2972
 Db 2859 GCAAGAGTCCAGCAGCAGTTCGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2918
 QY 2973 CTACACTCTCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3032
 Db 2919 CTACACTCTCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2978
 QY 3033 CCCCAGAGCAGTTCCTGCTCCCTTCCATCAGCAGCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3092
 Db 2979 CCCCAGAGCAGTTCCTGCTCCCTTCCATCAGCAGCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3038
 QY 3093 A 3093
 Db 3039 A 3039

RESULT 9
 AAS89721
 ID AAS89721 standard; cDNA; 3039 BP.
 XX
 AC AAS89721:
 XX
 XX
 DF 13-FEB-2002 (first entry)
 XX
 DB DNA encoding novel human diagnostic protein #25525.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX Homo sapiens.
 OS
 XX WO200175067-A2.
 PN
 XX 11-OCT-2001.
 PD
 XX 30-MAR-2001; 2001MO-US06631.
 PF
 XX 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0645167.
 XX
 PA (HYSE-) HYSEQ INC.
 PI Drmanac RT, Liu C, Tang YF.
 DR
 DR MPI; 2001-639362/73.
 DR P-PSDB; ABG25334.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 XX Claim 1; SEQ ID No 25525; 103bp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes.
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 XX
 SQ Sequence 3039 BP; 741 A; 869 C; 781 G; 648 T; 0 other;
 Query Match 71.8%; Score 2221.8; DB 23; Length 3039;
 Best Local Similarity 91.2%; Pred. No. 0;
 Matches 2408; Conservative 0; Mismatches 167; Indels 66; Gaps 2;

639 AGTGGCTCAGGTTTGAAGATGATATGGGAGATCTCAAGAGTCTCGGAGAAACAGTG 698
 819 GAGGTGTTCTCTGAAGCCGCGCTGTAAGTCTCAGTCTCTGAGACTCATTTTATTT 878
 699 GAGGTGTTCTCTGAAGCCGCGCTGTAAGTCTCAGTCTCTGAGACTCATTTTATTT 758
 879 CAACATTCCTCAGGAGATTACAGATGATGATGATGATGATGATGATGATGATGAT 938
 759 CAACATTCCTCAGGAGATTACAGATGATGATGATGATGATGATGATGATGATGAT 818
 939 AAGCTTTTACACCTTATACAGATGATGATGATGATGATGATGATGATGATGATGAT 998
 819 AAGCTTTTACACCTTATACAGATGATGATGATGATGATGATGATGATGATGATGAT 878
 999 TGACATTCGAGGTTTCTACTGAGATCAAGAGAAAGAGAGTCTCTATTCACCTG 1058
 879 TGACATTCGAGGTTTCTACTGAGATCAAGAGAAAGAGAGTCTCTATTCACCTG 938
 1059 GACACAGATTCCTGATGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1118
 939 GACACAGATTCCTGATGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 998
 1119 CTCCTTAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1178
 999 CTCCTTAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1058
 1179 GACGACCCGCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1238
 1059 GACGACCCGCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1118
 1239 AACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1298
 1119 AACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1178
 1299 GAATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1358
 1179 GAATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1238
 1359 AATGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1418
 1239 AATGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1298
 1419 CTCTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1478
 1299 CTCTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1358
 1479 CAGAGCAAGCAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1538
 1359 CAGAGCAAGCAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1418
 1539 CCGGTGGAACAGCAGTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1598
 1419 CCGGTGGAACAGCAGTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1478
 1599 TGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1653
 1479 TGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1538
 1654 ACTTTGAGCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1713
 1539 AGGCTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1598
 1714 TTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1773
 1599 ACTATGAG 1658
 1774 ACGGCTCAG 1794
 1659 AGGGGTGAG 1718
 1795 -----TGAAGGAG 1832
 1719 GTCTTACAGCGTTAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1778

CC the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

XX Sequence 3041 BP; 804 A; 886 C; 714 G; 637 T; 0 other;

Query Match 70.6%; Score 2182.4; DB 22; Length 3041;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2183; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

910 CSTATCAAGCGCGTATGTTGCTGCGAAGCTTTTCTACACCTTATACAGATCCCT 969
1 CGATCAACGGGCAATGATGTTGCTGCGAAGCTTTTCTACACCTTATACAGATCCCT 60
970 GGGTGTGACGTGTGCTGCTATGACATGCTTGAACATTTGCCAGTGTTTTACTGGAGATTG 1029
61 GGGTGTGACGTGTGCTGCTATGACATGCTTGAACATTTGCCAGTGTTTTACTGGAGATTG 120
1030 AAGGAACAGAAAGTCTGATGCTGATGCTGACACCGATGCTGATGACAGATTCCTAG 1089
121 AAGGAACAGAAAGTCTGATGCTGATGCTGACACCGATGCTGATGACAGATTCCTAG 180
1090 CCCAGGCGAGGTGCTGCTGCTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1149
181 CCCAGGCGAGGTGCTGCTGCTGCTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
1150 TTCCCTGATGATACCTGAACTTCAATCAAGACGACACCGCTGATGATGACAGATGCCC 1209
241 TTCCCTGATGATACCTGAACTTCAATCAAGACGACACCGCTGATGATGACAGATGCCC 300
1210 TTCCCTGATGATACCTGAACTTCAATCAAGACGATGATGATGATGATGATGATGATGATGAT 1269
301 TTCCCTGATGATACCTGAACTTCAATCAAGACGATGATGATGATGATGATGATGATGATGAT 360
1270 GCATGAGACACAGCTCTGCGGCAATATCAGAAATCAGATGCTGCTGCTGCTGCTGCTGCTGCT 1329
361 GCATGAGACACAGCTCTGCGGCAATATCAGAAATCAGATGCTGCTGCTGCTGCTGCTGCTGCT 420
1330 AAGGAATCATCTTGAAGTTTGGCCAGAAATAGTGGTTTCTAAATGACAGC 1389
421 AAGGAATCATCTTGAAGTTTGGCCAGAAATAGTGGTTTCTAAATGACAGC 480
1390 CTTTCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1449
481 CTTTCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
1450 GACAAAAGATCATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1509
541 GACAAAAGATCATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
1510 TCTACCTGTGTGATTAAGGTTCCCTTGGCCGATGATGATGATGATGATGATGATGATGATGAT 1569
601 TCTACCTGTGTGATTAAGGTTCCCTTGGCCGATGATGATGATGATGATGATGATGATGATGAT 660
1570 ACGTGTATGCTTCCAGAGACCATATTTGATGATGATTAAGGAAGGATGATGATGATGATGATGAT 1629
661 ACGTGTATGCTTCCAGAGACCATATTTGATGATGATTAAGGAAGGATGATGATGATGATGATGAT 720
1630 CATTTATCACCAACAGACAGATGATTTTGAAGAGATGATGATGATGATGATGATGATGATGAT 1689
721 CATTTATCACCAACAGACAGATGATTTTGAAGAGATGATGATGATGATGATGATGATGATGAT 780
1690 GGTCTGGGGAGTGTCAATTCCTTTTGGCACTGATGATGATGATGATGATGATGATGATGATGAT 1749
781 GGTCTGGGGAGTGTCAATTCCTTTTGGCACTGATGATGATGATGATGATGATGATGATGATGAT 840
1750 CCGAGCAACCAACATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1809
841 CCGAGCAACCAACATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900

1810 CTGACATGGAAGCATCTGCTTGTACTGCTGACAGACAGACACCTTTGGGGGAGTGTCT 1869
901 CTGACATGGAAGCATCTGCTTGTACTGCTGACAGACAGACACCTTTGGGGGAGTGTCT 960
1870 TCCCATTAATCACCAGACAGAAAGGAGATGATGCGGAAGTACTCAAGAGCCAGCAG 1929
961 TCCCATTAATCACCAGACAGAAAGGAGATGATGCGGAAGTACTCAAGAGCCAGCAG 1020
1930 CAGCTGTGCTCCGCTGACCTCTTGGCCATGATGATGATGATGATGATGATGATGATGATGATGAT 1989
1021 CAGCTGTGCTCCGCTGACCTCTTGGCCATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
1990 GTCTTCTGGGAGTACACCTCTTACTGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 2049
1081 GTCTTCTGGGAGTACACCTCTTACTGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 1140
2050 GTGACAGCAGAAAGAGAGAGTCAACCCACTGCGCGCGGAGCTCTCATGAGCAGCTGAC 2109
1141 GTGACAGCAGAAAGAGAGTCAACCCACTGCGCGCGGAGCTCTCATGAGCAGCTGAC 1200
2110 AAGCTGAGGCTCTTGGGAGACTCAATCCAAAGACCCAAAGCCGAGGCTATCTC 2169
1201 AAGCTGAGGCTCTTGGGAGACTCAATCCAAAGACCCAAAGCCGAGGCTATCTC 1260
2170 AGCCACTATGACAAAGGCAAGCTGCGCACTGCGGAGCAGACAGGCGCAAGATGCTCAT 2229
1261 AGCCACTATGACAAAGGCAAGCTGCGCACTGCGGAGCAGACAGGCGCAAGATGCTCAT 1320
2230 AAGGACAGCAGCAGCAGCAGCTGAGCTGAGCGGCTCTCCCAAGAGTCAACCCAGC 2289
1321 AAGGACAGCAGCAGCAGCAGCTGAGCTGAGCGGCTCTCCCAAGAGTCAACCCAGC 1380
2290 CTGACAG 2349
1381 CTGACAG 1440
2350 ATCAATGCTGCAAAAGGAGATGAG 2409
1441 ATCAATGCTGCAAAAGGAGATGAG 1500
2410 CCCCTGCGGCTCTCCCAAGCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2469
1501 CCCCTGCGGCTCTCCCAAGCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
2470 GGTCTACAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2529
1561 GGTCTACAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
2530 GAGGACAGGCGGCAACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2589
1621 GAGGACAGGCGGCAACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1680
2590 CCAACCATGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2649
1681 CCAACCATGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1740
2650 CCGGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2709
1741 CCGGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
2710 CTGGAATGACACCTCTCTCTGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2769
1801 CTGGAATGACACCTCTCTCTGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1860
2770 TCGCTCAGAGAAAGCAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2829
1861 TCGCTCAGAGAAAGCAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1920
2830 TCTCTCACTCTCTCAAAAGCAGAGCTTGGCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2889
1921 TCTCTCACTCTCTCAAAAGCAGAGCTTGGCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
2890 CAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2949

DB 1981 CAGAGGGTGCATCCATCAGAGTGCAGAGCTCCAGCATCTGGCCAGCGTACTGTC 2040
 QY 2950 TCGAGGACGCCAGCCTCAAGCCCTACACACTCAGCAAAAGTGGGGCTGAAGGCTACG 3009
 DB 2041 TCGAGGACGCCAGCCTCAAGCCCTACACACTCAGCAAAAGTGGGGCTGAAGGCTACG 2100
 QY 3010 CCGTGGTAAAGCCGAGGAGTACGCCCCCAACCATCTTGGCTCCCTTCACATCATG 3069
 DB 2101 CCGTGGTAAAGCCGAGGAGTACGCCCCCAACCATCTTGGCTCCCTTCACATCATG 2160
 QY 3070 AAGCCCAATGATGCTGTACATTA 3093
 DB 2161 AAGCCCAATGATGCTGTACATTA 2184

RESULT 11
 AAA93630
 ID AAA93630 standard; cDNA; 1890 BP.
 XX
 AC AAA93630;
 DT 16-JAN-2001 (first entry)
 DE Human semaphorin protein-like splice variant SECX PCR2.1-2864933 cDNA.
 XX
 KW SECX protein; human; secreted; membrane-associated; cancer;
 KW proliferation regulator; differentiation regulator; non-malignant tumour;
 KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
 KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
 KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
 KW neurological disease; Alzheimer's disease; trauma; wounding;
 KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;
 KW anti-HIV; antiinflammatory; antiarthritic; antiatherosclerotic;
 KW neuroprotective; vulnery; antiallergic; antimicrobial; cardiant;
 KW dermatological; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX MO200053742-A2.
 PN 14-SEP-2000.
 PD 09-MAR-2000; 2000MO-US06280.
 PE 09-MAR-1999; 99US-0123667.
 XX PR 08-MAR-2000; 2000US-0123667.
 PA (CURA-) CURAGEN CORP.
 PI Shinkets RA;
 DR WPI: 2000-594318/56.
 DR P-PSDB; AAB23043.
 PT Novel human membrane associated or secreted polypeptides and
 PT polynucleotides useful for diagnosis, prevention and treatment of
 PT pathological states such as cancer, immune, cardiovascular and
 PT neurological disorders -
 PS Claim 3; Fig 15; 151pp; English.
 XX Sequences AAA93616-A93631 and AAA93673-A93676 represent nucleic acids
 CC which encode human SECX proteins (AAB23029-B23048). The SECX proteins
 CC of the invention are either secreted or membrane-associated proteins
 CC and act as regulator of cellular proliferation and differentiation. SECX
 CC proteins or nucleotides are useful for diagnosing the presence of, or
 CC predisposition to, a disease associated with altered levels of SECX
 CC compounds and nucleotides. The SECX proteins are also useful to screen
 CC compounds that modulate SECX activity or expression. The interaction of
 CC a SECX protein with other cellular proteins may be useful to modulate
 CC the activity of a partner protein, cellular proliferation, cellular
 CC differentiation and cell survival. SECX nucleotides are useful for the

CC recombinant expression of SECX protein, and may be used to detect SECX mRNA
 CC or genetic lesions in the SECX gene. They may also be used to modulate
 CC SECX expression (e.g., using antisense oligonucleotides). SECX nucleic
 CC acid sequences are also useful for identifying a cell or tissue type in
 CC a biological sample, and in forensic biology. SECX primers or probes are
 CC useful for detecting the presence of SECX nucleotides and for screening
 CC tissue cultures for contamination. Diseases that may be treated or
 CC prevented using SECX proteins or nucleotides include cancer (e.g.,
 CC colorectal carcinoma, prostate cancer), benign tumours, immune disorders
 CC (including autoimmune diseases, cancer), transplant rejection, allergies, AIDS,
 CC infections, inflammatory disorders, arthritis, haematopoietic disorders,
 CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,
 CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g.,
 CC surgical or traumatic wounds, spinal cord injury), and skeletal
 CC disorders.
 XX
 SQ Sequence 1890 BP; 535 A; 426 C; 463 G; 466 T; 0 other;

Query Match 60.8%; Score 1881.6; DB 21; Length 1890;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1884; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 49 GGGGCGGTTTCCCGAAGATTCTGAGCCCAATCAGATTTCGATGCGCACTATACAAA 108
 DB 1 GGATCGGTTTCCCGAAGATTCTGAGCCCAATCAGATTTCGATGCGCACTATACAAA 60
 QY 109 CAGTATCCGAGTGTGTGGCCACAGACCGAGACACACACAGACGACGCTG 168
 DB 61 CAGTATCCGAGTGTGTGGCCACAGACCGAGACACACACAGACGACGCTG 120
 QY 169 GACATCCAGATGATATATGATTCATGAAAGGAAACCCCTGATGCTGCTGGGACATAT 228
 DB 121 GACATCCAGATGATATATGATTCATGAAAGGAAACCCCTGATGCTGCTGGGACATAT 180
 QY 229 TATAGCTGTGATATAGACACATCACACAGGAAAGAAATTTATGTGACAAAACCTGACA 288
 DB 181 TATAGCTGTGATATAGACACATCACACAGGAAAGAAATTTATGTGACAAAACCTGACA 240
 QY 289 TGGAAATCTAGACAGCCGATGATGACACATGAGAAATGAGGAAACATATAGATGAG 348
 DB 241 TGGAAATCTAGACAGCCGATGATGACACATGAGAAATGAGGAAACATATAGATGAG 300
 QY 349 TGGCAACACTTATTTAAAGTCTCTTAAAGAAAGAGATGATGATGATGATGATGATG 408
 DB 301 TGGCAACACTTATTTAAAGTCTCTTAAAGAAAGAGATGATGATGATGATGATGATG 360
 QY 409 ACTAATGCTTCAACCCCTCTGACAGAAACCTATATAGATGATGATGATGATGATGATG 468
 DB 361 ACTAATGCTTCAACCCCTCTGACAGAAACCTATATAGATGATGATGATGATGATGATG 420
 QY 469 GATGAATTCAGCGGAATGGCCAGATGCCATATGATGATGATGATGATGATGATGATG 528
 DB 421 GATGAATTCAGCGGAATGGCCAGATGCCATATGATGATGATGATGATGATGATGATG 480
 QY 529 TTTCAGATGAGAAACCTATATCTAGCCACAGTACTGACTCTCTTCCATTGACGAGTC 588
 DB 481 TTTCAGATGAGAAACCTATATCTAGCCACAGTACTGACTCTCTTCCATTGACGAGTC 540
 QY 589 ATTACCGGAGTCTTGAGAAAGCCCTACCCCTCGGACCCCTCAAGACAGATTAATGAG 648
 DB 541 ATTACCGGAGTCTTGAGAAAGCCCTACCCCTCGGACCCCTCAAGACAGATTAATGAG 600
 QY 649 TTGAAGAAACCACTATCTTGTCAAGCGGTGATGATGATGATGATGATGATGATGATG 708
 DB 601 TTGAAGAAACCACTATCTTGTCAAGCGGTGATGATGATGATGATGATGATGATGATG 660
 QY 709 AGGGAATATAGCACTGAGATTAACACCATGAGGAAGGTACTTTCCACAGATGAGCTGAC 768
 DB 661 AGGGAATATAGCACTGAGATTAACACCATGAGGAAGGTACTTTCCACAGATGAGCTGAC 720
 QY 769 GTTTGTAAGATGATATGAGGAGATCTCAAGAGTCTGAGGAAACAGTGGAGTGGCTTC 828
 DB 721 GTTTGTAAGATGATATGAGGAGATCTCAAGAGTCTGAGGAAACAGTGGAGTGGCTTC 780

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QY 829 CTGAGGCGGCTTGAAGTCTCAGTCCGAGAGCTCATTTTATTTCAACATCTC 888
    |||||
Db 781 CTGAGGCGGCTTGAAGTCTCAGTCCGAGAGCTCATTTTATTTCAACATCTC 840
QY 889 CAGGAGTTACAGATGTATTCATCAACGGGCGTGTGCTTCCGCAACGTTTCT 948
    |||||
Db 841 CAGGAGTTACAGATGTATTCATCAACGGGCGTGTGCTTCCGCAACGTTTCT 900
QY 949 ACACCTTATPACAGCATCCCTGGGTCTGCGAGTCTGTGCCATATACATGCTTGCATTTGCC 1008
    |||||
Db 901 ACACCTTATPACAGCATCCCTGGGTCTGCGAGTCTGTGCCATATACATGCTTGCATTTGCC 960
QY 1009 AGTGTCTTCTGAGGATTCAGAGAACAGAGCTTCCTGATTCACCTGGACACAGTT 1068
    |||||
Db 961 AGTGTCTTCTGAGGATTCAGAGAACAGAGCTTCCTGATTCACCTGGACACAGTT 1020
QY 1069 CCTGATGAAACAGATTCCTTAAGCCAGCCAGGTGTGCTGTGCTGCTCCTCTTGA 1128
    |||||
Db 1021 CCTGATGAAACAGATTCCTTAAGCCAGCCAGGTGTGCTGTGCTGCTCCTCTTGA 1080
QY 1129 AGATATGCAACCTTCACATGAGTTCCTGATGATACCTGTAATTCATCAAGAGCACCG 1188
    |||||
Db 1081 AGATATGCAACCTTCACATGAGTTCCTGATGATACCTGTAATTCATCAAGAGCACCG 1140
QY 1189 CTCATGATGAGGAGGAGGCGCTCCATCTTCACAGGCGCATGTTCCGAGACATGATGTC 1248
    |||||
Db 1141 CTCATGATGAGGAGGAGGCGCTCCATCTTCACAGGCGCATGTTCCGAGACATGATGTC 1200
QY 1249 AGATACCGCCTTACCAAAATTCAGAGTGTGAGACACAGCTCTGGGCCATATCAGATCAGACT 1308
    |||||
Db 1201 AGATACCGCCTTACCAAAATTCAGAGTGTGAGACACAGCTCTGGGCCATATCAGATCAGACT 1260
QY 1309 GTGGTCTTCTGAGGATCAGAGAGAGGATATCTTGAAGTCTTGGCCAGAAATAGAAAT 1368
    |||||
Db 1261 GTGGTCTTCTGAGGATCAGAGAGAGGATATCTTGAAGTCTTGGCCAGAAATAGAAAT 1320
QY 1369 AGTGTCTTCTAAATGACAGCTTCTCTGAGGAGATGATGTTTCAACTCTGAAAAA 1428
    |||||
Db 1321 AGTGTCTTCTAAATGACAGCTTCTCTGAGGAGATGATGTTTCAACTCTGAAAAA 1380
QY 1429 TGCAGCTATGATGAGTGCAGAGACAAAAGATCATGGGATCATGCTGTGAGACAGCAAGC 1488
    |||||
Db 1381 TGCAGCTATGATGAGTGCAGAGACAAAAGATCATGGGATCATGCTGTGAGACAGCAAGC 1440
QY 1489 AGCTCTCTGATATGTTGCGTCTCTCACTGTGTGATAAAGTTCCTTGGCCGGTGTGAA 1548
    |||||
Db 1441 AGCTCTCTGATATGTTGCGTCTCTCACTGTGTGATAAAGTTCCTTGGCCGGTGTGAA 1500
QY 1549 CGACATGGGAAGTGTAAAAAAACCTGTATTGCTCTCAGAGACCAATTTTGGATGATA 1608
    |||||
Db 1501 CGACATGGGAAGTGTAAAAAAACCTGTATTGCTCTCAGAGACCAATTTTGGATGATA 1560
QY 1609 AAGGAGGTGTGCTGCTGACGCTTATTCACCCAAACAGACAGTACTTTTGGACAGAGAC 1668
    |||||
Db 1561 AAGGAGGTGTGCTGCTGACGCTTATTCACCCAAACAGACAGTACTTTTGGACAGAGAC 1620
QY 1669 ATAGAGGTGTCATPACAGATGATGCTGGGGAGCTGTCACAAATTCCTTGTGGCACTGAT 1728
    |||||
Db 1621 ATAGAGGTGTCATPACAGATGATGCTGGGGAGCTGTCACAAATTCCTTGTGGCACTGAT 1680
QY 1729 GGGCATTCACATTCCTCTTCCAGACAGCAACACATCATGATTCGACGGCTCAAGAGGGG 1788
    |||||
Db 1681 GGGCATTCACATTCCTCTTCCAGACAGCAACACATCATGATTCGACGGCTCAAGAGGGG 1740
QY 1789 TATGAGTCTAGGGGAGGAATGCTGAGTGTGAGATCTGTGCTTGAATCTACCTGACAGCACA 1848
    |||||
Db 1741 TATGAGTCTAGGGGAGGAATGCTGAGTGTGAGATCTGTGCTTGAATCTACCTGACAGCACA 1800
QY 1849 GACCTTTGGGGGAGGCTCTTCCCATATATCAACCAAGCAAGAGAGGAGTGTGGGGA 1908
    |||||
Db 1801 GACCTTTGGGGGAGGCTCTTCCCATATATCAACCAAGCAAGAGAGGAGTGTGGGGA 1860

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QY 1909 AGTTACCTCAAGGCCACGACAGCTGG 1936
    |||||
Db 1861 AGTTACCTCAAGGCCACGACAGCTGG 1888

RESULT 12
AAH15834
ID AAH15834 standard; cDNA; 2293 BP.
XX
AC AAH15834;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:14327.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 8; SEQ ID 14327; 2537pp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification, where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination
CC of the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialized methods. AAH03166 to AAH13628 and
CC AAH13632 to AAH18742 represent human cDNA sequences; AAH92446 to
CC AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 2293 BP; 579 A; 713 C; 581 G; 420 T; 0 other;

```

Query Match 59.0%; Score 1824.4; DB 22; Length 2293;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1825; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1268 TTGAGTGGACACAGCTGCTGGGCCATATCAGAAATCACACTGTGTTTCTCGGATCAG 1327
1 TTGCATATGGACACAGCTGCTGGGCCATATCAGAAATCACACTGTGTTTCTCGGATCAG 60
1328 AGAAGGAAATCATCTTGAAGTTTGGCCAGAAATAGTGGTTTCTTAATGACA 1387
61 AGAAGGAAATCATCTTGAAGTTTGGCCAGAAATAGTGGTTTCTTAATGACA 120
1388 GCGTTTCTGGAGGAGTGAAGTTTACACTGTGAATAATGACCTGTATGAGGTG 1447
121 GCGTTTCTGGAGGAGTGAAGTTTACACTGTGAATAATGACCTGTATGAGGTG 180
1448 AAGACAAAAGATCATGGGATGAGCTGAGACAGACAGACAGACAGCTCTGTATGTCGT 1507
181 AAGACAAAAGATCATGGGATGAGCTGAGACAGACAGACAGACAGCTCTGTATGTCGT 240
1508 TCTCTACCTGTGTGAATAAGTTCCCTTGGCCGGTGTAGACGACATGGGAAGTTGAAA 1567
241 TCTCTACCTGTGTGAATAAGTTCCCTTGGCCGGTGTAGACGACATGGGAAGTTGAAA 300
1568 AAGCTGTATGCTGCTGAGACAGACATATTGTGATGATTAAGAAAGGTGCTGCA 1627
301 AAGCTGTATGCTGCTGAGACAGACATATTGTGATGATTAAGAAAGGTGCTGCA 360
1628 GCCATTTATCACCACAGACAGACTGACTTTTGGAGAGACATAGAGCGTGGCAATACAG 1687
361 GCCATTTATCACCACAGACAGACTGACTTTTGGAGAGACATAGAGCGTGGCAATACAG 420
1688 ATGGTCTGGGGAGCTGACAAATTCCTTGTGACATGAAATGGGCAATCCCTCT 1747
421 ATGGTCTGGGGAGCTGACAAATTCCTTGTGACATGAAATGGGCAATCCCTCT 480
1748 TGCCGACGACAAACCATCATGATTCGACGGCTCAAGAGGGTATGATGATGAGGAGAA 1807
481 TGCCGACGACAAACCATCATGATTCGACGGCTCAAGAGGGTATGATGATGAGGAGAA 540
1808 TGTGAGCTGGAAGCATCTGCTTACTACCTACACAGACAGACAGCTTTGGGGGAGTGT 1867
541 TGTGAGCTGGAAGCATCTGCTTACTACCTACACAGACAGACAGCTTTGGGGGAGTGT 600
1868 CTGCCATATATCACAAGACAAAGAGGAGTGAATGGGAAAGTTAACTCAAGAGCAGC 1927
601 CTGCCATATATCACAAGACAAAGAGGAGTGAATGGGAAAGTTAACTCAAGAGCAGC 660
1928 ACCAGCTGTGCTCCGTCACCTCTTGCCATGTCAGTCAATCTGCTTGTGTCATGGGG 1987
661 ACCAGCTGTGCTCCGTCACCTCTTGCCATGTCAGTCAATCTGCTTGTGTCATGGGG 720
1988 CCGTCTCTGGGGATCACCCTGTACTGCTCTGTGATCATCGGCGCAAGAGCTGCTG 2047
721 CCGTCTCTGGGGATCACCCTGTACTGCTCTGTGATCATCGGCGCAAGAGCTGCTG 780
2048 TGGTGACGCGCAAGAGAGAGAGTCAACCACTGCGCGCGGCTCCATAGACAGCTCA 2107
781 TGGTGACGCGCAAGAGAGAGAGTCAACCACTGCGCGCGGCTCCATAGACAGCTCA 840
2108 CCAAGCTCAGCGGCTCTTTGGGGACACTAATCCAAAGAACCCAAAGCGGAGGCTATCC 2167
841 CCAAGCTCAGCGGCTCTTTGGGGACACTAATCCAAAGAACCCAAAGCGGAGGCTATCC 900
2168 TCACGCCACTCATGCAACAGCGCAAGCTGCGCAATCCCGCAACAGCGCAAGGTGTCA 2227
901 TCACGCCACTCATGCAACAGCGCAAGCTGCGCAATCCCGCAACAGCGCAAGGTGTCA 960
2228 TTTAAGGACGACACACACCTGAGACTGAGCGGCTCCACACCCAGAGTCAACCCCAA 2287
961 TTTAAGGACGACACACACCTGAGACTGAGCGGCTCCACACCCAGAGTCAACCCCAA 1020
2288 CGCTGCAAGCAAG 2347
1021 CGCTGCAAGCAAG 1080

2348 TCATCATGCTCTGCACAAAGAGATGCCCCCATGGGCTCCCTGTGATTCCTCCAGGACC 2407
1081 TCATCATGCTCTGCACAAAGAGATGCCCCCATGGGCTCCCTGTGATTCCTCCAGGACC 1140
2408 TGCCCCCTGGGGCTCCCTCCAGCATATCCAGAGGTGGTGGCTGCTCCATACAGCAGC 2467
1141 TGCCCCCTGGGGCTCCCTCCAGCATATCCAGAGGTGGTGGCTGCTCCATACAGCAGC 1200
2468 AGGGCTACAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2527
1201 AGGGCTACAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
2528 TGGAGGACCAAGCGCCGACACTGAGATTAAGACCTCAAGAGAACTTCAGAGAGAA 2587
1261 TGGAGGACCAAGCGCCGACACTGAGATTAAGACCTCAAGAGAACTTCAGAGAGAA 1320
2588 GTGCCAACCATGGGGTGAACCTGTGTGAGAGAACTGTGAGAGAACTGTGAGAGAACTGT 2647
1321 GTGCCAACCATGGGGTGAACCTGTGTGAGAGAACTGTGAGAGAACTGTGAGAGAACTGT 1380
2648 AGCGGAGAGCTCCCTGGGTCGCCCGGAGCTCCCTGTCTCAGACCGGTCTAAGCAAGC 2707
1381 AGCGGAGAGCTCCCTGGGTCGCCCGGAGCTCCCTGTCTCAGACCGGTCTAAGCAAGC 1440
2708 GGTGGAATGACCACTCTCTTCTTACGGGGTGTACTATAAGAGAGGTACCCAGCA 2767
1441 GGTGGAATGACCACTCTCTTCTTACGGGGTGTACTATAAGAGAGGTACCCAGCA 1500
2768 ACTGCTCAGAGAAAGCCACAGGAGCACTCTCAAAAGAAACAACTACTCTCTCA 2827
1501 ACTGCTCAGAGAAAGCCACAGGAGCACTCTCAAAAGAAACAACTACTCTCTCA 1560
2828 ATTCTCTCACT 2887
1561 ATTCTCTCACT 1620
2888 CGCAGAGGGTGAAGCTCATGAGTGCACAGCTCCAGGCTCTGAGAGAGAGAGAGAGAG 2947
1621 CGCAGAGGGTGAAGCTCATGAGTGCACAGCTCCAGGCTCTGAGAGAGAGAGAGAGAG 1680
2948 TCTGAGGAGAGCCGACCTCTACAGCTCTACAACTGATGAAAGTGGGGCTGAAGGTA 3007
1681 TCTGAGGAGAGCCGACCTCTACAGCTCTACAACTGATGAAAGTGGGGCTGAAGGTA 1740
3008 CGCCCTGCTAAAGCGGAGAGTACCCCGCAACCATCTTGTCTCCCTTTCACATCCA 3067
1741 CGCCCTGCTAAAGCGGAGAGTACCCCGCAACCATCTTGTCTCCCTTTCACATCCA 1800
3068 TGAAGCCCAATGATGCTGTACATTA 3093
1801 TGAAGCCCAATGATGCTGTACATTA 1826

RESULT 13
AAK94365
ID AAK94365 standard; cDNA; 2227 BP.
AAK94365;
06-NOV-2001 (first entry)
XX
Human full-length cDNA, seq ID NO: 3087.
DE
Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX
Homo sapiens.
OS
XX
EP1130094-A2.
FN
XX
05-SEP-2001.
PD
XX
07-JUL-2000; 2000EP-0114089.
PF
XX

PR 08-JUL-1999: 99UP-0194486-
PR 11-JAN-2000: 2000UP-018774.
PR 02-MAY-2000: 2000UP-0183765.
XX
XX (HELI-) HELIX RES INST.
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y,
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
XX MPI: 2001-524255/58.
DR F-PSDB: AAM93444.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their
PT use in genetic manipulation -
XX
XX claim 8: SEQ ID NO 3087; 1380bp + sequence listing; English.
XX
XX The invention relates to primers for synthesizing full length cDNA
XX clones. 830 cDNA molecules encoding a human protein have been
XX isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
XX molecules have been determined. Primers for synthesizing the full length
XX cDNA are useful for clarifying the function of the protein encoded by
XX the cDNA. The full length clones were obtained by construction of full
XX length enriched cDNA libraries that were synthesised by the oligo-capping
XX method. The primers enable the production of the full length cDNA easily
XX without any special methods. The present sequence is a full length
XX human cDNA of the invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in CD-ROM format directly from EPO.
SQ
SQ Sequence 2227 BP; 567 A; 700 C; 560 G; 400 T; 0 other;
Query Match 56.38; Score 1742.4; DB 22; Length 2227;
Best local Similarity 99.9%; Pred. No. 0;
Matches 1743; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1350 TTGGGCGAAGTGAATAGTGGTTTCTAATGACAGCCTTTCTCGAGAGATGAG 1409
DB 1 TTGGGCGAAGTGAATAGTGGTTTCTAATGACAGCCTTTCTCGAGAGATGAG 60
QY 1410 TGTTCACACTCTGAAAAATGACGATGATGAGTGGAGACAAAAGATCATGGCAT 1469
DB 61 TGTTCACACTCTGAAAAATGACGATGATGAGTGGAGACAAAAGATCATGGCAT 120
QY 1470 GCAGCTGACAGAGACAGACAGCTCTGATGATGAGTGGAGACAAAAGATCATGGCAT 1529
DB 121 GCAGCTGACAGAGACAGACAGCTCTGATGATGAGTGGAGACAAAAGATCATGGCAT 180
QY 1530 TCCCTTGGCGGCTGTGACAGACATGGGAAGTGTAAAAAACCCTGATATGGCTCCAGAGA 1589
DB 181 TCCCTTGGCGGCTGTGACAGACATGGGAAGTGTAAAAAACCCTGATATGGCTCCAGAGA 240
QY 1590 CCCATATTTGATGATTAAGGAAGTGGTGGCTGACAGCATTTATCAACCAACAGAG 1649
DB 241 CCCATATTTGATGATTAAGGAAGTGGTGGCTGACAGCATTTATCAACCAACAGAG 300
QY 1650 ACTGACTTTGAGAGAGACATAGAGCGTGGCATATAGATGCTGGGGGAGCTGTCAAA 1709
DB 301 ACTGACTTTGAGAGAGACATAGAGCGTGGCATATAGATGCTGGGGGAGCTGTCAAA 360
QY 1710 TTCTTTTGGCAGTGAATGGCATTTCCCTCTTGGCCAGACACACACATCATGA 1769
DB 361 TTCTTTTGGCAGTGAATGGCATTTCCCTCTTGGCCAGACACACACATCATGA 420
QY 1770 TTGACAGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGAGCTGGAAGCATCTCT 1829
DB 421 TTGACAGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGAGCTGGAAGCATCTCT 480
QY 1830 TGACTCAGCTAGAGAGACAGACCCCTTTGGGGGAGTGTCTCCCTAATACCAAGACAA 1889
DB 481 TGACTCAGCTAGAGAGACAGACCCCTTTGGGGGAGTGTCTCCCTAATACCAAGACAA 540
QY 1890 GAAGGAGTGAATGGGAAGTTACCTCAAAAGCCAGACAGCTGTTCCCGTACCT 1949

DB 541 GAAGGAGTGAATGGGAAGTTACCTCAAAAGCCAGACAGCTGTTCCCGTACCT 600
QY 1950 CTTGGGCAATGACATCATCTGCTTCTCATGAGGGGCGCTCTTCTCGGGCATCAACCT 2009
DB 601 CTTGGGCAATGACATCATCTGCTTCTCATGAGGGGCGCTCTTCTCGGGCATCAACCT 660
QY 2010 CTACTCGCTGTGTGATCATGCGGCAAGACGTGCTGTGTGACGCGCAAGAGAAAGA 2069
DB 661 CTACTCGCTGTGTGATCATGCGGCAAGACGTGCTGTGTGACGCGCAAGAGAAAGA 720
QY 2070 GCTCACCACACTGCGCGGGGCTCCATGAGACCGTCCACACGCTCAGCGGCTCTTGG 2129
DB 721 GCTCACCACACTGCGCGGGGCTCCATGAGACCGTCCACACGCTCAGCGGCTCTTGG 780
QY 2130 GGACACTCATCCAAAGACCCAAAGCGGAGGCGCATCTCCACCTCATGACAAACGG 2189
DB 781 GGACACTCATCCAAAGACCCAAAGCGGAGGCGCATCTCCACCTCATGACAAACGG 840
QY 2190 CAAGCTGCGCACTCCGCGCAACAGCGCCAAAGATGCTCATTAAGACAGACCATCACT 2249
DB 841 CAAGCTGCGCACTCCGCGCAACAGCGCCAAAGATGCTCATTAAGACAGACCATCACT 900
QY 2250 GGAAGCTGAGCGGCTCCCGCACCCAGAGTCAACCCCAAGCGCTGACAGAGAGAGCC 2309
DB 901 GGAAGCTGAGCGGCTCCCGCACCCAGAGTCAACCCCAAGCGCTGACAGAGAGAGCC 960
QY 2310 CAGCGCGGAGCAGCGGAGTGGAGAGAGAACCCAACTCATCATCTCTGACAAAGA 2369
DB 961 CAGCGCGGAGCAGCGGAGTGGAGAGAGAACCCAACTCATCATCTCTGACAAAGA 1020
QY 2370 CATGCCCCCATGAGGCTCCCGTGTATTCACAGGACCTGCGGGGCTCTCCCGAG 2429
DB 1021 CATGCCCCCATGAGGCTCCCGTGTATTCACAGGACCTGCGGGGCTCTCCCGAG 1080
QY 2430 CCACATCCCAAGCGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2489
DB 1081 CCACATCCCAAGCGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 2490 GGAACAGCCCAAAATGAGAGAGTGGCCAGAGTGGCTGAGAGACAGCGCCGCAACT 2549
DB 1141 GGAACAGCCCAAAATGAGAGAGTGGCCAGAGTGGCTGAGAGACAGCGCCGCAACT 1200
QY 2550 GGAATATTAAGACATCAAGGAACATCTCAGAGAGAGTGGCCAGAGTGGGAGAACT 2609
DB 1201 GGAATATTAAGACATCAAGGAACATCTCAGAGAGAGTGGCCAGAGTGGGAGAACT 1260
QY 2610 TGTGAGAACCTTGAGACAGCTGCGCCCAAAAGTTCACAGCGGAGAGGCTCTCGGCTC 2669
DB 1261 TGTGAGAACCTTGAGACAGCTGCGCCCAAAAGTTCACAGCGGAGAGGCTCTCGGCTC 1320
QY 2670 CCGGAGAGCTCCCTGTCTCAGACCGGTCTAAGCAAGGCTGGAAATGACCACTCTC 2729
DB 1321 CCGGAGAGCTCCCTGTCTCAGACCGGTCTAAGCAAGGCTGGAAATGACCACTCTC 1380
QY 2730 TTCTAGAGGGGTGCTCTAAGAGAGTATCCCAAGCACTGCTCAGAGAGAGCACCA 2789
DB 1381 TTCTAGAGGGGTGCTCTAAGAGAGTATCCCAAGCACTGCTCAGAGAGAGCACCA 1440
QY 2790 GGCCACACTCTCAAAAGAAACACACTAATCTCTCAATCTCTCACTCTCTCAAGAA 2849
DB 1441 GGCCACACTCTCAAAAGAAACACACTAATCTCTCAATCTCTCTCACTCTCTCAAGAA 1500
QY 2850 CCAGAGCTTTGGCAGGGAGAGACACCGCGCGCGCGCGCGCGCGAGAGGAGTCCATCA 2909
DB 1501 CCAGAGCTTTGGCAGGGAGAGACACCGCGCGCGCGCGCGCGAGAGGAGTCCATCA 1560
QY 2910 GGTGACAGCTCCCGAGCATCTGGCAGAGCGCTGACTGCTGAGAGAGCCAGGCTCAA 2969
DB 1561 GGTGACAGCTCCCGAGCATCTGGCAGAGCGCTGACTGCTGAGAGAGCCAGGCTCAA 1620
QY 2970 GGCCTAACAACTACTAGACAAAGTCCGGGCTGAAGCTGACGCTCTGCTTAAGCGGAGCT 3029

Db 1621 CGCCTACACTGACAGAGTGGGCGTGAAGCGTACCCCTGCTAAAGCCGAGCT 1680
QY 3030 ACCCCCAACCATCTCTTGTCCCTTCCACATCAAGAGCCCAATGATGCGTAC 3089
Db 1681 ACCCCCAACCATCTCTTGTCCCTTCCACATCAAGAGCCCAATGATGCGTAC 1740
QY 3090 ATAA 3093
Db 1741 ATAA 1744

RESULT 14
AAH17861
ID AAH17861 standard; cDNA; 2306 BP.
AC AAH17861;
DT 26-JUN-2001 (first entry)
DE Human cDNA sequence SEQ ID NO:17567.
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
OS Homo sapiens.
PN EP1074617-A2.
PD 07-FEB-2001.
PF 28-JUL-2000; 2000EP-0116126.
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
PA (HELI-) HELIX RES INST.
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
PS Claim 8; SEQ ID 17567; 2537pp + CD ROM; English.
XX The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination
CC of the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to
CC AAH93893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

XX
SQ Sequence 2306 BP; 579 A; 739 C; 577 G; 411 T; 0 other;
QY
Query Match 53.9%; Score 1666.4; DB 22; Length 2306;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1667; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1426 AATGCGATGATGAGTGCAGAGCAAAAGATCATGCGCATGAGCGACAGAGCA 1485
Db 166 AGATGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 225
QY 1486 AGCAGCTCTCTGTATGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1545
Db 226 AGCAGCTCTCTGTATGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 285
QY 1546 GAACGACATGGAAGTGTAAAAAACCCTGTATGCTGTCTGTCTGTCTGTCTGTCTGT 1605
Db 286 GAACGACATGGAAGTGTAAAAAACCCTGTATGCTGTCTGTCTGTCTGTCTGTCTGT 345
QY 1606 ATAAAGAAAGTGTGCTGCTGACGCAATTTATCACCACAGAGACTGACTTTTGAGCAG 1665
Db 346 ATAAAGAAAGTGTGCTGCTGACGCAATTTATCACCACAGAGACTGACTTTTGAGCAG 405
QY 1666 GACATAGAGCGTGGCAATACAGATGCTGTGGGAGCTGTACAAATTCCTTTGTGGCAGTG 1725
Db 406 GACATAGAGCGTGGCAATACAGATGCTGTGGGAGCTGTACAAATTCCTTTGTGGCAGTG 465
QY 1726 AATGGGATTCGATTCCTTCCCTTGGCCAGCAACCATCATGATTCGAGCGCTCAAGAG 1785
Db 466 AATGGGATTCGATTCCTTCCCTTGGCCAGCAACCATCATGATTCGAGCGCTCAAGAG 525
QY 1786 GCGTATGAGTCTAGGGGAGAAATGCTGAGTGTGAGCATGCTGTGACTACCTGACAGC 1845
Db 526 GCGTATGAGTCTAGGGGAGAAATGCTGAGTGTGAGCATGCTGTGACTACCTGACAGC 585
QY 1846 ACAGACCCCTTGGGGGAGTGTCTTCCCATATCACCACAAAGAAAGGAGATTCGG 1905
Db 586 ACAGACCCCTTGGGGGAGTGTCTTCCCATATCACCACAAAGAAAGGAGATTCGG 645
QY 1906 GAAAGTATCCCAAAAGGCGACGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1965
Db 646 GAAAGTATCCCAAAAGGCGACGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 705
QY 1966 ATCTGCTTTCGTCATGAGGGGCGCTTCTCGGGGATCACCCTGTACCTGCTGTGAT 2025
Db 706 ATCTGCTTTCGTCATGAGGGGCGCTTCTCGGGGATCACCCTGTACCTGCTGTGAT 765
QY 2026 CATCGGCGAAAGACGTGCTGTGTGTGACGCGCAAGAGAGAGCTCACCCACTCGCGC 2085
Db 766 CATCGGCGAAAGACGTGCTGTGTGTGACGCGCAAGAGAGAGCTCACCCACTCGCGC 825
QY 2086 CGGGGCTCCATGACGACGTCACCAAGCTGAGCGGCTCTTGGGGACACTCATCCAA 2145
Db 826 CGGGGCTCCATGACGACGTCACCAAGCTGAGCGGCTCTTGGGGACACTCATCCAA 885
QY 2146 GACCCAAAGCGGAGGCGATCTCAGCGCACTCATGCAACAGGCAAGCTGCCACTGCC 2205
Db 886 GACCCAAAGCGGAGGCGATCTCAGCGCACTCATGCAACAGGCAAGCTGCCACTGCC 945
QY 2206 GGCACACGCGCAAGATGCTATTAAGACAGACGACGACGCTGAGACTGAGCGGCTC 2265
Db 946 GGCACACGCGCAAGATGCTATTAAGACAGACGACGACGCTGAGACTGAGCGGCTC 1005
QY 2266 CCCACCCAGAGTACACCCCAAGCTGACGAGAGGAGGCCAGGCCGCGGACGCCG 2325
Db 1006 CCCACCCAGAGTACACCCCAAGCTGACGAGAGGAGGCCAGGCCGCGGACGCCG 1065
QY 2326 GAGTGGAGAGGAACCAAGCTTCAATGCTGTGCAAAAGGACATGCTGCTGCTGCTGCTG 2385
Db 1066 GAGTGGAGAGGAACCAAGCTTCAATGCTGTGCAAAAGGACATGCTGCTGCTGCTGCTG 1125
QY 2386 TCCCTGATTCACGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2445

Db	1126	TTCCCTCTGATTTTCCACAGACCTTCGCCCTTCGGGGCTTCGCCACGCCATCTCCCAAGGTG	1185
QY	2446	GTGGTCTCTGCCATCTACGCGACGAGGGGCTACAGCATGATGATCGTGGACACGCCAAATG	2505
Db	1186	GTGGTCTCTGCCATCTACGCGACGAGGGGCTACAGCATGATGATGATCGTGGACACGCCAAATG	1245
QY	2506	AGGAGGTTGGCCCATGATGGGGCTGGAGGACCGAGCGCCACACTGGAGTATTAAGCATC	2565
Db	1246	AGGAGGTTGGCCCATGATGGGGCTGGAGGACCGAGCGCCACACTGGAGTATTAAGCATC	1305
QY	2566	AAGGAACTCTCAGACGACGAAGAGTCCGAACTATGGGGTGAACCTTGTGGAAACCTGAGC	2625
Db	1306	AAGGAACTCTCAGACGACGAAGAGTCCGAACTATGGGGTGAACCTTGTGGAAACCTGAGC	1365
QY	2626	AGCCTGCCCCCAAGTTCCACAGCGGGGAGGCTCTCTGGGTCCCCCGGGAGCCTCCCTG	2685
Db	1366	AGCCTGCCCCCAAGTTCCACAGCGGGGAGGCTCTCTGGGTCCCCCGGGAGCCTCCCTG	1425
QY	2686	TCTCAGACGGTCTAAGCAAGCGGCTGGAATGACACACTCTCTTCTCTAAGGGGTTGAC	2745
Db	1426	TCTCAGACGGTCTAAGCAAGCGGCTGGAATGACACACTCTCTTCTCTAAGGGGTTGAC	1485
QY	2746	TATTAAGAGAGCTACCCGACGACTCGTCAAGAAAGCCACGAGGCCACACTCTCAAA	2805
Db	1486	TATTAAGAGAGAGCTACCCGACGACTCGTCAAGAAAGCCACGAGGCCACACTCTCAAA	1545
QY	2806	AGAAACAACACTAATCTCTCCAACTCTCTCTACCTCTCCAGAAACCAAGGTTGGCAGG	2865
Db	1546	AGAAACAACACTAATCTCTCCAACTCTCTCTACCTCTCCAGAAACCAAGGTTGGCAGG	1605
QY	2866	GGAGACAACCCGCGCGCCGCGCCGACAGAGGTTGACTTCACAGGTGCACAGCTCCAG	2925
Db	1606	GGAGACAACCCGCGCGCGCCGCGCCGACAGAGGTTGACTTCACAGGTGCACAGCTCCAG	1665
QY	2926	CCATCTGGCCAGGGCGGTGACTGTCTGGAGGACGCCAGGCCACAGGCTTACAGTCACTG	2985
Db	1666	CCATCTGGCCAGGGCGGTGACTGTCTGGAGGACGCCAGGCCACAGGCTTACAGTCACTG	1725
QY	2986	ACAAAGGTGGGGCTGAAGCGGTAGCGCCCTGCTAAAGCCGGAAGTACCCGCCAAACCATGC	3045
Db	1726	ACAAAGGTGGGGCTGAAGCGGTAGCGCCCTGCTAAAGCCGGAAGTACCCGCCAAACCATGC	1785
QY	3046	TTTCTCTCCCTTTTCCACATCCATGAAAGCCCAATGATGGGTACTATA 3093	
Db	1786	TTTCTCTCCCTTTTCCACATCCATGAAAGCCCAATGATGGGTACTATA 1833	
RESULT 15			
ID	AA568253	standard; CDNA: 2592 BP.	
AC	AA568253;		
XX			
DE	13-FEB-2002 (first entry)		
XX			
DE	DNA encoding novel human diagnostic protein #4057.		
XX			
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;		
KW	food supplement; medical imaging; diagnostic; genetic disorder; ss.		
OS	Homo sapiens.		
XX			
PN	WO200175067-A2.		
XX			
PD	11-OCT-2001.		
XX			
PF	30-MAR-2001; 2001WO-0508631.		
XX			
PR	31-MAR-2000; 2000US-0540217.		
XX			
XX	23-AUG-2000; 2000US-0649167.		
PA	(HYSE-) HYSEQ INC.		
XX			

XX	Dmanac RT, Liu C, Tang YT:
DR	WPI: 2001-639362/73.
DR	P-P5DB; ABG04066.
XX	New isolated polynucleotide and encoded polypeptides, useful in
PT	diagnostics, forensics, gene mapping, identification of mutations
PT	responsible for genetic disorders or other traits and to assess
PT	biodiversity -
XX	
XX	Claim 1: SEQ ID No 4057; 103pp; English.
PS	
CC	The invention relates to isolated polynucleotide (I) and
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC	and gene mapping, and in recombinant production of (II). The
CC	polynucleotides are also used in diagnostics as expressed sequence tags
CC	for identifying expressed genes. (I) is useful in gene therapy techniques
CC	to restore normal activity of (II) or to treat disease states involving
CC	(II). (II) is useful for generating antibodies against it, detecting or
CC	quantitating a polypeptide in tissue, as molecular weight markers and as
CC	a food supplement. (II) and its binding partners are useful in medical
CC	imaging of sites expressing (II). (I) and (II) are useful for treating
CC	disorders involving aberrant protein expression or biological activity.
CC	The polypeptide and polynucleotide sequences have applications in
CC	diagnostics, forensics, gene mapping, identification of mutations
CC	responsible for genetic disorders or other traits to assess biodiversity
CC	and to produce other types of data and products dependent on DNA and
CC	amino acid sequencing sequences. AAS64197-AAS94564 represent novel human
CC	diagnostic coding sequences of the invention.
CC	Note: The sequence data for this patent did not appear in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_poc_sequences.
SQ	
XX	Sequence 2592 BP; 655 A; 754 C; 659 G; 524 T; 0 other;
Query Match	51.5%; Score 1592; DB 23; Length 2592;
Best Local Similarity	84.3%; Pred. No. 0;
Matches 1809; Conservative	0; Mismatches 325; Indels 12; Gaps 1;
QY	960 CAGCATCCCTGGGTCTGCATGTCGTGGCCTATGACATGCTTGACATGCCAGTGTTTTAC 1019
DB	
447	CAGCATCCCTGGGTCTGCATGTCGTGGCCTATGACATGCTTGACATGCCAGTGTTTTAC 506
QY	1020 TGGGAGATTCAAGGAACAAGAAGTCCTCGATTCCACTGGACACCAGTTCCTGATGAAGC 1079
DB	
507	TGGGAGATTCAAGGAACAAGAAGTCCTCGATTCCACTGGACACCAGTTCCTGATGAAGC 566
QY	1080 AGTTCCTAAGCCAGGCCAGGCTGTGCTGTGCTACTCCTCTTAGAAAGATATGCAAC 1139
DB	
567	AGTTCCTAAGCCAGGCCAGGCTGTGCTGTGCTACTCCTCTTAGAAAGATATGCAAC 626
QY	1140 CTCCAATAGTTCCTGTATGTAATACCGAATTCATACAGACGACCCGGCTCAGATGA 1199
DB	
627	CTCCAAATAGTTCCTGTATGTAATACCGAATTCATACAGACGACCCGGCTCAGATGA 686
QY	1200 GGCAATGGCCCTCCATCTTCAACAGGCGCATGTGTTCTGAGAACAAATGTCAGATACGGCT 1259
DB	
687	GGCAATGGCCCTCCATCTTCAACAGGCGCATGTGTTCTGAGAACAAATGTCAGATACGGCT 746
QY	1260 TACCAAATTCGATGAGACACAGCTGCTGGGCGCAATACAGATACAGTGGTTTTTC 1319
DB	
747	TACCAAATTCGATGAGACACAGCTGCTGGGCGCAATACAGATACAGTGGTTTTTC 806
QY	1320 GGGATCAGAGAGGGAATCATCTTGAAATTTTGGCCAGAAATAGAAAATACTGGTTTTCT 1379
DB	
807	GGGATCAGAGAGGGAATCATCTTGAAATTTTGGCCAGAAATAGAAAATACTGGTTTTCT 866
QY	1380 AAATGACAGCCTTTTCTCGAGAGAGATAGTGTTTACAACTCTGAAAAATGACACTTGA 1439
DB	
867	AAATGACAGCCTTTTCTCGAGAGAGATAGTGTTTACAACTCTGAAAAATGAGAGCAC 926
QY	1440 TGGAGTCGAAAGCAAAAGATCATGGGCTCAGCTGAGTGAAGACCAAGCACTCTCTGTA 1499

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Db      927  CGAATAACCTGTGAGGGTATACCATTTCTTAAACCTGTGCAAGCTAGTTTCTGATCAC  986
QY      1500  TGTGGTCTCTTACCTGTGTGATAAAGTTCCCTTGGCCGGGTGGAACGACATGGAA  1559
Db      987  ACTTAGAAGAACAGTGGTGGAGGAGAAAACATATTGGTTCGCCCATATGTTGCACCC  1046
QY      1560  GTTATAAAAAACCTGATTTGCCCTCCAGAACCCATTTGTGGATGATTAAGAAAGTGG  1619
Db      1047  CTTCAATAGACACTTTTGTCCATGTCTACTATCTTTCTGGCAAGAAACCTCTGCCGTGT  1106
QY      1620  TGGCTTCAGCCATTATTCACCCAACAGCACTGACTTTTGGACAGCATATAGAGCTGG  1679
Db      1107  GACTGGTGGATGTAAGGTAAAGGACACCGAGATGATCTTTGCCATATGCTCTATGTT  1166
QY      1680  CAATACAGATGCTGTGGGGGACTGTCAATTCCTTTGTGGCATGTAATGGGCATTCAG  1739
Db      1167  GCGTGCCAGGATATGGTTCAGAGGTGCAAGGAACGSGTATTTACTGCTTACACATCAA  1226
QY      1740  TTCCCTCTTGGCCAGACACACCATCATATTCAGAGGCTCAAGAGGGGTATGAGTCTAG  1799
Db      1227  AACCCGGGCCAAGGAGGAATAGCAAAAGACTCTTGAGACCTGGGGCCCATGGCCCT  1286
QY      1800  GGGAGGATGCTGAGACTGGAAGCATCTGTTGACTCACTGACCTGACAGCACA-----  1850
Db      1287  CGAGCCCTTGCCCCCTCGGTTGGTTAAAGGCAAAACCTTTCCCAAGGAGGCTCCG  1346
QY      1851  ---CCCTTTGGGGGACGTGTTCTTCCATATACCAAGACAGAAAGGAGTATTGGGA  1907
Db      1347  GTGGCCACAAGGGGGTCTCGGAAAAGATCCCAACTCGAAAGCCCAAGAGTGTTCGGGA  1406
QY      1908  AATTACCTCAAAAGGCGACGACAGCTGGTTCCCGTACCCCTTGGGCAATTCAGTCAT  1967
Db      1407  AAGTTACCTCAAAAGGCGACGACAGCTGGTTCCCGTACCCCTTGGGCAATTCAGTCAT  1466
QY      1968  CCGGCTTCTGTCATGGGGGCGGTCTTCTCGGGCATCACCGTCTACTGGCTGTGATCA  2027
Db      1467  CTTGGCTTCTGTCATGGGGGCGGTCTTCTCGGGCATCACCGTCTACTGGCTGTGATCA  1526
QY      2028  TCGGGCGAAAGAGCTGGTGTGTGTGTCAGCGCAAGGAGAGGAGTCAACCCTCGCGCG  2087
Db      1527  TCGGGCGAAAGAGCTGGTGTGTGTGTCAGCGCAAGGAGAGGAGTCAACCCTCGCGCG  1586
QY      2088  GGGCTCATGAGAGGCTACCAAGCTCAGCGGCTCTTTGGGGACACTCAATCCAAGA  2147
Db      1587  GGGCTCATGAGAGGCTACCAAGCTCAGCGGCTCTTTGGGGACACTCAATCCAAGA  1546
QY      2148  CCCAAAGCCGAGGCAATCCTCAAGCTCAGGCTCATGCAACGCGCAAGCTCGCACTCCG  2207
Db      1647  CCCAAAGCCGAGGCAATCCTCAAGCTCAGGCTCATGCAACGCGCAAGCTCGCACTCCG  1706
QY      2208  CAACAGGCGCAAGATGCTCTTAAAGCAGCAGCAGCAGCAGCTGACCTGAGGCGCTCC  2267
Db      1707  CAACAGGCGCAAGATGCTCTTAAAGCAGCAGCAGCAGCAGCTGACCTGAGGCGCTCC  1766
QY      2268  CACCCAGAGTCAACCCCAAGCTGAGCAGAGCGGAAGCCAGCGCGGAGCGGAG  2327
Db      1767  CACCCAGAGTCAACCCCAAGCTGAGCAGAGGAGGAAGCCAGCGCGGAGCGGAG  1826
QY      2328  GTGGAGAGGAGAACCAAGCTCATCAATGCTTGCAAAAGAGACATGCCCCCATGGGCTC  2387
Db      1827  GTGGAGAGGAGAACCAAGCTCATCAATGCTTGCAAAAGAGACATGCCCCCATGGGCTC  1886
QY      2388  CCTGTGATTCACAGGACCTGCCCTGGGGGCTCCCGCAGGCACATGCCCAAGCGTGT  2447
Db      1887  CCTGTGATTCACAGGACCTGCCCTGGGGGCTCCCGCAGGCACATGCCCAAGCGTGT  1946
QY      2448  GGTCTGTCATCAGCAGAGGAGCTACAGCATGAGTACGTGAGCCAGCCCAAAATGAG  2507
Db      1947  GGTCTGTCATCAGCAGAGGAGCTACAGCATGAGTACGTGAGCCAGCCCAAAATGAG  2006
QY      2508  CGAGTGGCCAGATGCGCTGAGAGCAAGGCGCCACACTGAGTATTAAGACATCAA  2567

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Db      2007  CGAGTGGCCAGATGGCGCTGGAGAGCCAGCGCCACACTGAGTATTAAGACATCAA  2066
QY      2568  GGAACATCTCAGCAGAGAAAGTCCCAACCATGGGGGTAACCTTGTGAGAACCTGGACAG  2627
Db      2067  GGAACATCTCAGCAGAGAAAGTCCCAACCATGGGGGTAACCTTGTGAGAACCTGGACAG  2126
QY      2628  CCTGGCCCCCAAGTTCACAGCGGGAGGCTCCCTGGGGTCCCGCGGAGCCTCCCTGTC  2687
Db      2127  CCTGGCCCCCAAGTTCACAGCGGGAGGCTCCCTGGGGTCCCGCGGAGCCTCCCTGTC  2186
QY      2688  TCAGACGGGTCAAGCAGCGGCTGGAATGCAACACTCTCTCTCTACGGGTTACTTA  2747
Db      2187  TCAGACGGGTCAAGCAGCGGCTGGAATGCAACACTCTCTCTCTACGGGTTACTTA  2246
QY      2748  TAAGAGACTACCCCAAGCACTGCTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  2807
Db      2247  TAAGAGACTACCCCAAGCACTGCTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  2306
QY      2808  AAACAACACTACTCTCTCAATTCCTCTCACTCTCTCACTCTCTCAAGAACAGAGCTTGG  2867
Db      2307  AAACAACACTACTCTCTCAATTCCTCTCACTCTCTCACTCTCTCAAGAACAGAGCTTGG  2366
QY      2868  AGACAAACCCGCGCCCGCCCGCAGAGGAGTGAATCTCATTCAGAGTGCACAGTCCAGCC  2927
Db      2367  AGACAAACCCGCGCCCGCCCGCAGAGGAGTGAATCTCATTCAGAGTGCACAGTCCAGCC  2426
QY      2928  ATCTGGCCAGGCGGTGACTGTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  2987
Db      2427  ATCTGGCCAGGCGGTGACTGTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  2486
QY      2988  AAGGTGGGGCTGAAGCGTACGCGCTCGCTAAAGCCGGAGCGTACCCGCCAACCATCTTT  3047
Db      2487  AAGGTGGGGCTGAAGCGTACGCGCTCGCTAAAGCCGGAGCGTACCCGCCAACCATCTTT  2546
QY      3048  TGCTCCCTTTCCACATTCATGAAGCCCAATGATGGGTGATCAATAA  3093
Db      2547  TGCTCCCTTTCCACATTCATGAAGCCCAATGATGGGTGATCAATAA  2592

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Search completed: September 30, 2003, 16:58:34
 Job time : 808.168 secs


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Db      312 CCCCCACGTCACAGGAGTGGGTAACAGAGAAAGTACCTGAGATCTAACCCAGC 371
QY      307 GATGTAGACATGCAAGATGAAAGGAAACATAGAGATGATGCCACACTTATATA 366
Db      372 GACATTAACGATGTCGATGAAGGCAACAGAGGAGGAGTGTGAACCTTCGTAAG 431
QY      367 GTCTCTCTAAAGAAAACATGATGATGTTGCTGTGGAAGTATGCTTCAACCTT 426
Db      432 GTGCTCTCTCTGAGAGAGTCCAGCCCTTTGTGTGCGGTTCCAAACCCCTCA 491
QY      427 TCTGCAAGAACTATAGATGATGATGATGGAACATTGGGGATGATTCAGCGAAT 486
Db      492 GTGTGGCCAACTACAGCATAGACCCCTGACCCCGTGGAACAACTACACCGGTA 551
QY      487 GCGAGATGCCAATGATGCAACATGCCAAGCTGCACTGTTGCAGATGGAAGAACTA 546
Db      552 GCGCGCTGCGCGTAGACACCCAGCAGCCAAATGTTGCCCTCTTCTCTGACGGAGT 611
QY      547 TACTACAGCAGTACTGACTGCTTCCCTGCAATGACAGTCAATTCACGGAGCTTGA 606
Db      612 TTCCAGAGTACTGTTACCGACTTCTAGCATGATGATGCTCATACGCAAGCTGG 671
QY      607 GAAAGCCCTACCTGCGGAGCCGTCAGACAGATTCAAATGTTGAAGAACATCTTT 666
Db      672 GACAGGCCACCCCTGCGACACCTGAAACATGACTCCAAAGTGTTCAAAGCCCTT 731
QY      667 GTTCAAGCCGTGATTACGAGATTAATCTACTTCTCTTCAAGGAAATAGCAGTGA 726
Db      732 GTGATAGCGGTGAGAGTGGGACACCATGCTACTTCTCTCGGGAGATGGAGTGA 791
QY      727 TATACACCAATGAGAAAGTAGTTTCCCAAGATGCGTCAAGTGTGTGAATGATG 786
Db      792 TTTAACTACTGAGAGAGTGTGTGTCTCCGCGGTGCGGAGTGTGCAAGACGAG 851
QY      787 GAGAGATCTAAAGAGTCCCTGGAAGAAACATGACGCTCTCTGAAAGGCGGCTGAA 846
Db      852 GAGAGGTCCTCCCGCGGTGTGAGAAAGCATGAGCGTCTCTGAAAGGCGGCTGAA 911
QY      847 TGCTAGTCTCTGAGAGACTCTATTTTATTTTCAACTCTCCAGGCACTTACAGATG 906
Db      912 TGCTCTGTACCCGAGACTCCCATTTTCTACTTCAAGTGTGACGGCTGACAGGGG 971
QY      907 ATTGCTATCAAGCGGCTGATGTTGCTCTGCAACGTTTCTACACTTAAACAGATC 966
Db      972 GTGAGCTCTGAGGCGCGCGGTGCTGCTGCGGTTTTCACGCGCCAGCAAGATC 1031
QY      967 CCGGCTGCTGAGTCTGCTGATGATGACATGCTTGAACATGCTTCTTACTGAGAGA 1026
Db      1032 CTTGCTGCTGCTGCTGCTGCTTGAACATGACATGCTGCTGCTGCTGCTGCTG 1091
QY      1027 TTCAAGAGACAGAAAGTCTGATTTGCACTGACACCAAGTCTGATGAAGAGTCT 1086
Db      1092 TTCCGAGAGACAGAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1151
QY      1087 AAGCCCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1146
Db      1152 CGACCCCGCGCGGCTCT-----GCGACGCGCGCGGAGTGCATGACATGCTCCAGC 1205
QY      1147 GAGTTCCTGATGATACCTGATACCTGATACCTGATACCTGATACCTGATACCTGAT 1206
Db      1206 GCTTTCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1265
QY      1207 CCGTTCATCTTCAACAGGCGATGCTGCTGGAAGCAATGATGATGATGATGATGATG 1266
Db      1266 CCGTTCGCTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1325
QY      1267 ATTGAGTGAACAGAGTGTGAGGCGATGATGATGATGATGATGATGATGATGATG 1326
Db      1326 GTGCTGTGAGAGTGTGAGGCGCGCGCTGAGGAGCAACGACGCTGTCTGCTGCT 1385
QY      1327 GAGAGAGATCATCTTGAAGTCTTT-----GCGCAGATAGAGAAATAGTGTCTTA 1380
Db      1386 GAGGCGGAGAGGCTCTCAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1445

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QY      1381 AATGACAGCCTTTCTCTGAGAGATGAGTGTTTACACTGAAAAATGAC-----C 1434
Db      1446 GGGCTCAGTGTCTCTCTGAGAGATGAGTGTTTACACTGAGGCGGAGAGTGTGAGC 1505
QY      1435 TATGATGAGTGAAGACAAAGAGATGATGAGTGTGAGTGTGAGTGTGAGTGTG 1494
Db      1506 GGGGCTGAGAGACAGAGGAGCGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1565
QY      1495 CTGTATGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1554
Db      1566 CTGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1625
QY      1555 GGGAGTGTAAAAAACTGTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1614
Db      1626 TCGGCTGTATGAGAACTGTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1685
QY      1615 GGTGTGCTGCTGAGCCTATTAACAGACAGAGAGTGTGAGTGTGAGTGTGAGTGT 1674
Db      1686 GGTCT---CTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1742
QY      1675 CGTGCAATACAGATGATGCTGAGGAGCTG 1703
Db      1743 GGGGCGACAGACCTCAGGCTTAGGGAGCTG 1771

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RESULT 2
US-09-077-940A-1
: Sequence 1, Application US/09077940A
: Patent No. 6576441
: GENERAL INFORMATION:
: APPLICANT: KIMURA, Toru et al.
: TITLE OF INVENTION: NOVEL SEMAPHORIN 2 AND GENE ENCODING THE SAME
: FILE REFERENCE: 0020-4426P
: CURRENT APPLICATION NUMBER: US/09/077, 940A
: CURRENT FILING DATE: 1998-06-05
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1
: LENGTH: 3692
: TYPE: DNA
: ORGANISM: Rattus norvegicus
: FEATURE:
: NAME/KEY: 5' UTR
: LOCATION: (1)..(18)
: OTHER INFORMATION:
: NAME/KEY: CDS
: LOCATION: (19)..(2682)
: OTHER INFORMATION:
: NAME/KEY: 3' UTR
: LOCATION: (2683)..(3653)
: OTHER INFORMATION:
: NAME/KEY: POLYA-site
: LOCATION: (3654)..(3692)
: OTHER INFORMATION:
: US-09-077-940A-1

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Query Match      17.7%: Score 546.8; DB 4; Length 3692;
Best Local Similarity 60.3%: Pred. No. 2, Le-136;
Matches 1006; Conservative 0; Mismatches 632; Indels 30; Gaps 5;

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QY      57 TTCCAGAGATGATCTGAGCCAAATCAGTATTTGCGATGAGCACTATACAAAGATATCC 116
Db      99 TTTCACATGATGACCACTCCACATGATGATGATGATGATGATGATGATGATGATG 158
QY      117 GGTGTTTGTGGCCCAAGCCAGAGACGGAACACACACAGAGGCG-----ACAGGCTGGA 170
Db      159 CGTGTCTGTGGCAAGCGGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 218
QY      171 CATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 230
Db      219 CATCCAGAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 278

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[illegible]

Db	1353	AGTCTTCTCGTGGCTCTGAGGTGGCACAGTCTCAATTTCTTTGAAGGCCAATTTGGCCAG	1412
QY	1365	AAATAGTGGTTTCTAATATGACAGCCTTTTCTTGAGAGATGATGTTT-----A	1415
Db	1413	TGCTTCAGGGGACACAGGGGCCACACATCTTTTGGAGAGATTATGACCTAACCGGCCAGA	1472
QY	1416	CAACTCGAAATATGACGCTATGATGTGAGTGGAGACAAAAGATATCATGGGCATGACACT	1475
Db	1473	CAGGTGTGGACGATTCACAGCACTGCTGTGGATGTTGGGACACACGACTTCTGACACCTGGACT	1532
QY	1476	GGACAGAGCAACGACGCTCTCTGTATGTGTTGCCCTTCTACGTGTGATTAAGTTCCCTT	1535
Db	1533	AGATGTGTCGCCACAGTGGCTGTCTGTGGACGCTTCCCGCGTGTTGGTTCTTGTTGTTCCGT	1592
QY	1536	TGGCCGGTGTAAAGACATGTGGGAAGTGTAAAAAACCTGTTTGTGCTCCAGAGACCATA	1595
Db	1593	TGCCCGCTGCCAGCTGTACTCTGGGGTGCCATGAAGACATGTCATTTGGCAGCCACGAATCCATA	1655
QY	1596	TTGTGTGATGATTAAGGAGAGGTGTGTGCTCGAGGCCATTTATCACCACACAGACGACTGAC	1655
Db	1653	CTGGGGGTGGGGCCCCCGA---TGGGTCTCGATCTTCTCCAGACCGAGAACCCAGTGGCCAC	1700
QY	1656	TTTGTGACGACGACATAGACCTGGCATATACAGATGTGTGTGGGGGACTG	1703
Db	1710	GTTTTGGTGAAGATGTGTGTCGGGGCCCGACGACCTCTGGCTTAGTGAAGTGT	1757

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RESULT 3
US-09-254-594-5
; Sequence 5, Application US/09254594
; Patent No. 6560094
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru
; APPLICANT: KIKUCHI, Kaoru
; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
; FILE REFERENCE: 0020-4527P
; CURRENT APPLICATION NUMBER: US/09/254,594
; CURRENT FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 2790
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (..)()
; OTHER INFORMATION: Tissue type: Child Brain
; NAME/KEY: CDS
; LOCATION: (1)..(2790)
; OTHER INFORMATION: Identification Method: E
; NAME/KEY: misc_feature
; LOCATION: (..)()
; OTHER INFORMATION: Identification Method: P for resulting peptide
US-09-254-594-5

Query Match          14.3%; Score 443.6; DB 4; Length 2790;
Best local similarity 58.6%; Pred. No. 8.3e-109;
Matches 849; Conservative 0; Mismatches 584; Indels 15; Gaps 4

DY      164 GCCTGACATCCAGATGATTATGATCATGAAGCAACCCTTCATCTTGTCTGAGGGACC 223
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DY      179 GGCTGCACCTTCAGACATTCCTGACCTTGAAACCGGACCTTGCTAGTGGCTGCCGGGATC 238
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DY      224 ATATTATATCTGGTTAGTAGACACATCATCACACGGAAGAATAATTATTTAGCAAAAAC 283
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DY      239 ACCTTTTCTTCCTTCGATCTTCACAAGCGAAGAAAGAGAGGGGGGCTGTGCCAACAAAGT 298
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      284 TGACATGAATCTAGACAGGCCGATGTAGACATGCAGATGTGAAGGGAAAAACATAAGS 343
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DY      ANCTA--ACATGGAAGAACCAAGATGTGGAGAACTGCTGTAGCGGGAAAGCTGACGS 355

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QY 344 ATGAGTGCACCACTTTATTAAGTCTTCTTAAGAAAAACGATGATGCTGTGTCT 403
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Db 356 ATGAGTGCACCACTTTATTAAGTCTTCTTAAGAAAAACGATGATGCTGTGTCT 415
QY 404 GTGGAACTAATGCTTCAACCCCTTCTGAGAAAACATAAGATGATGATGAAACAT 463
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 416 GTGGAACTAATGCTTCAACCCCTTCTGAGAAAACATAAGATGATGATGAAACAT 475
QY 464 TGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 523
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 476 AGGATGAGAACTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 535
QY 524 CACTGTTGAGATGAGAAAACTATTAAGTCAAGCCAGTGAAGTGAAGTGAAGTGA 583
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 536 CCACTTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 595
QY 584 CAGTCAATTAAGGAGGAGTGTGAGAAAACCCCTACCTGGGAGCCGTCAGACGATG 643
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 596 CTGTAGTTTACAGAAAGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 655
QY 644 AATGTTGAAAGAACATCTTGTCAAGCCGTGATTAAGGAGATTAATATCTACTCT 703
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 656 AGTGGCTCGAGAGCCACACTTGTCCAGGCTTGGAGCATGAGACCATGCTACTCT 715
QY 704 TCTTCAGGAAATAGCAGTGAAGTATTAACACATGAGGAAAGTATTTTCCAGAGTGG 763
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 716 TCTTCGCGAGAGTCTGTGTGAGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGG 775
QY 764 CTGAGGTTTGAAGATGATGAGGAGGATCTCAAGAGTCTCGGAGAAACATGAGAGT 823
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 776 CCGAGATGATTAACGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 835
QY 824 CGTTCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 883
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 836 CTTTCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 895
QY 884 TTCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 943
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 896 TTTTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 955
QY 944 TTTTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1003
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 956 TACACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1015
QY 1004 TTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1063
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1016 TTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1075
QY 1064 CAGTTCCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1123
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1076 CTGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1135
QY 1124 TAGAAATATGCAACCTCCAAATGATGATGATGATGATGATGATGATGATGATG 1183
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1136 CTGCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1195
QY 1184 ACCCGCTATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1243
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1196 ACCCGCTATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1252
QY 1244 TGGTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1303
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1253 CTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1312
QY 1304 ACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1363
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1313 TCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1372
QY 1364 GAAATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1423
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1373 GCGGATCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1429
QY 1424 AAAAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1477

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Db 1430 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1489
QY 1478 ACAGAGCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1537
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Db 1490 ACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1549
QY 1538 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1597
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1550 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1609
QY 1598 GTGGATGG 1605
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Db 1610 GTGGATGG 1617

RESULT 4
US-09-254-594-4
; Sequence 4, Application US/09254594
; Patent No. 6566094
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru
; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
; FILE REFERENCE: 0020-4527P
; CURRENT APPLICATION NUMBER: US/09/254,594
; CURRENT FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 3432
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(3432)
; OTHER INFORMATION: Tissue Type: Child Brain
; NAME/KEY: 5'UTR
; LOCATION: (1)-(187)
; OTHER INFORMATION: Identification Method: E
; NAME/KEY: misc feature
; LOCATION: (188)-(2977)
; OTHER INFORMATION: CDS; Identification Method: E
; NAME/KEY: 3'UTR
; LOCATION: (2978)-(3407)
; OTHER INFORMATION: Identification Method: E
; NAME/KEY: polyA_signal
; LOCATION: (3408)-(3432)
; OTHER INFORMATION: Identification Method: E
US-09-254-594-4

Query Match 14.3%; Score 443.6; DB 4; Length 3432;
Best Local Similarity 58.6%; Pred. No. 9.2e-109;
Matches 849; Conservative 0; Mismatches 584; Indels 15; Gaps 4;

QY 164 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 223
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 366 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 425
QY 224 ATATTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 283
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 426 ACATTTCCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 485
QY 284 TGACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 343
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Db 486 ATCTA---ACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 542
QY 344 ATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 403
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 543 ATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 602
QY 404 GTGAACTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 463
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Db 603 GTGAGCAACTCATTCAGCCCTGTGTGCCGACGCTATGGGATTAATTCCTGTGAGCAGG 662
 QY 464 TCGGGGATGATTCAGGGGAATGGCCGATGCCCATATGATGCCAATGCCAAGCTGG 523
 Db 663 AGGGTGGGAACGTAGTGGGAGGCTGATGAGCCCTTGTATGCCACCAAGTCCAGCGTGG 722
 QY 524 CACTGTGTGAGATGAGAAACTATATACAGCCACAGTACTGACTGACTTCCATTCAGC 583
 Db 723 CCATCTTTGACAGAGGAGGAGCTGTACTCAGCCACAGCTGCGGATTTCCAGGCCGATATG 782
 QY 584 CAGTCATTTAOCGAGTCTTGGAGAAAGCCCTACCTGCGAGCCGTACAGCAGATTCAA 643
 Db 783 CTGTAGTTTACAGAAAGCTTGGGCCCCCAGCCCGCTCCGCTCCCAAGATATACCTCA 842
 QY 644 AATGTTGAAAGAACCTACTTTTGTAAAGCCGTGGATATACGGGATTTATATCTACTCT 703
 Db 843 AGTGGCTCCGAGAGCCACACTTTGTCCAGGCTTGGAGACATGAGACCATCTACTACTCT 902
 QY 704 TCTTCAGGGAATATGAGTGGATATTAACACATGAGGAAAGTATTTTCCAGAGCTGG 763
 Db 903 TCTTCCCGAGGCTCTGTGTGAGAGATGCTGGGCTGGGGAAGGTGCACTTCTCCCGCTAG 962
 QY 764 CTCAGGTTTGAAGATGATATGAGAGATCTCAAGAGTCTGAGAAACAGTGGACGT 823
 Db 963 CCGAGATATGTAACGTGACATGGCGGCTCGCTCGGGCTTGGACCGCAGCTGGACAT 1022
 QY 824 CGTTCGGAAGGCGCGCTTGAAGCTCAGTCTGAGTCCGAGACTCTATTTATTTTCAACA 883
 Db 1023 CCTTCGTAAGCTTGGCTCAACTGCTCTGTCCCTGGGAGCTACTACTTCTATTTTGTATG 1082
 QY 884 TTCTCCAGGAGATTAAGATGATGATGCTATCAACGGGCGTGTATGTTGCTCGCAACGT 943
 Db 1083 TTTTACAGGCTTGTACTGGGCTGTGAACCTGCAATGGCGCTGCTGCTCTTTGGGGTCT 1142
 QY 944 TTCTACACCTTATTAACAGCATCCCTGGGCTGTGCACTGTGCTCATGACATGCTTACA 1003
 Db 1143 TCACACCCCAACCAATGACATCCCTGCTGCTGCTGCTGCTGCTTACCTGATGAGTA 1202
 QY 1004 TTGCGAGTGTTTTACTGGGAGATTCAGAGAAAGATTCCTGATTCACCTGGAGAC 1063
 Db 1203 TTGAGCGTGGTGTGAGGGCAAGTTCAGAGAGCAGAGAGATGCTGGATGGGCTGTGACTC 1262
 QY 1064 CAGTTCCTGATGAAGAGAGTCTTAAGCCAGGCCAGGTTGCTGCTGCATCCTCTCT 1123
 Db 1263 CTGTGTCTGAGAGAGAGATTCCTCCACAGGCCAGAGATCCTGTGACAGAGAGAGGAG 1322
 QY 1124 TAGAAAGATATGCAACTCTCAATGATGTTCCCTGATGATACCTGAACTTCATCAAGAGC 1183
 Db 1323 CTGCTGTCTCTCTCTCTCCGAGACCTCCGTGATGATGCTGCTGCTTCAATCAAGGCTC 1382
 QY 1184 ACCGCTCATGATGAGGAGGAGGCGCTCCATCTTCAAGAGGCGATGGTTCCGAGAACAA 1243
 Db 1383 ACCGCTCTGTGAGCCCGCTGACCACTGTACCACTCAAGCC---TCTACTCACTCA 1439
 QY 1244 TGGTGAATACCGCTTACCAAAATTTGCAAGTGGACACAGCTGCGGCCCATATTCGAATC 1303
 Db 1440 CTAGAGAGGCGCTACTGACCAAGATGATGATGGATGGATGGCTGGTCCCACTAACA 1499
 QY 1304 ACATGTGATTTTCTGGGATCAGAGAGGAATATCTTGAAGTTTGGCCAAATATAG 1363
 Db 1500 TCACAGTATATGTTCTGCTCCATCCATGATGGAGAGTCTGTAAGGTGCTGAGCCCAAGGTG 1559
 QY 1364 GAAATAGTGTTTTAAATGACAGCCCTTCTGAGAGATGATGTTTCAACTCTG 1423
 Db 1560 GCGCATCCGG---GGGACCTGAGCCCATCTCTGGAAGAGATTTGATGCTACAGCCCTG 1616
 QY 1424 AAAATGCACTATATGAGAGTGC-----AAGACAAAAGATCATGGGACATGACGCTGG 1477
 Db 1617 CCGGATGAGTGGAGAGGAGGAGCCCAAGCAAGCAAGGATCATAGGGCTGAGAGCTGG 1676
 QY 1478 ACAGAGCAAGAGCTCTCTGATATGTTGGCTCTCTACCTGCTGATTAAGGTTCCCTTG 1537
 Db 1677 ACACGAGGCTCAGAGGCTTTTGTGGCTTTTGTGGCTGATGTTGCTACCTCCCTCA 1736

QY 1538 GCCGCTGTGAACGATGGAAGTGTAAAAAAACCTGATTTGCTCCAGAGACCATATT 1587
 Db 1737 GCCGCTGTGCCCGGATATGGGCGCTGTCAAGAGAGCTGTTGGCTTCAAGACCATTACT 1796
 QY 1598 GTGATGG 1605
 Db 1797 GTGATGG 1804
 RESULT 5
 US-09-254-594-2
 : Sequence 2, Application US/09254594
 : Patent No. 6566094
 : GENERAL INFORMATION:
 : APPLICANT: KIMURA, Toru
 : APPLICANT: KIKUCHI, Kaoru
 : TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
 : FILE REFERENCE: 0020-4527P
 : CURRENT APPLICATION NUMBER: US/09/254,594
 : CURRENT FILING DATE: 1999-05-11
 : NUMBER OF SEQ ID NOS: 13
 : SOFTWARE: PatentIn version 3.0
 : SEQ ID NO 2
 : LENGTH: 2787
 : TYPE: DNA
 : ORGANISM: Rattus norvegicus
 : FEATURE:
 : NAME/KEY: misc.feature
 : LOCATION: (1)..(2787)
 : OTHER INFORMATION: Tissue Type: Brain
 : NAME/KEY: CDS
 : LOCATION: (1)..(2787)
 : OTHER INFORMATION: Identification Method: E
 : NAME/KEY: misc.feature
 : LOCATION: (1)..(1)
 : OTHER INFORMATION: Identification Method: p for resulting peptide
 US-09-254-594-2
 Query Match 12.0%; Score 369.8; DB 4; Length 2787;
 Best Local Similarity 55.9%; Pred. No. 5e-89;
 Matches 811; Conservative 0; Mismatches 622; Indels 18; Gaps 5;
 QY 164 GCGTGACATCCAGATGATATATGATCATGAGACGGAACCTCTACTGTTGCTGTAGGAGC 223
 Db 176 GCGTGACATCCAGATGATATATGATCATGAGACGGAACCTCTGTTGCTGTAGGAGATC 235
 QY 224 ATATTATATCTGTTATATATGACATGACACAGGAAAGAAATTTATTAGCAAAAAC 283
 Db 236 AGCTTTCTCTGATCTTCAAGCCACAGAGAAAGGAGGCGCTGTGCGCCAAAGT 295
 QY 284 TGACATGGAATCTAGACAGGCGGATGTAGACACATGACAGANTGAAAGGAAACATTAAG 343
 Db 296 T---TCTGACATGGGAGGAGCCAAAGACATGAGAAATTTGCTGCGGGGAAAGCTGACG 352
 QY 344 ATGATGCCACAACTTTATTAAGTCTTCTTAAGAAAGAAACCATGATGATGATGTTGTCT 403
 Db 353 AGCAATGCTACAAACATACATCCGTTGTTGTTCCCTGAGGCTCGCAGACATCTCTGCT 412
 QY 404 GNGAGAACTAATGCTTCAACCTCTCTGAGAGAACTATAGATGATGATGATGATGAT 463
 Db 413 GNGAGAACTAATGCTTCAACCTCTCTGAGAGAACTATAGATGATGATGATGATGAT 472
 QY 464 TCGGAGTGAATTCAGCGGATGCGGAGATGCCAGATGCCATATGATGCCAAACATGCCAGTGG 523
 Db 473 AGGGAGAGAGGCTGATGATGGGCAAGCTCGATGCGCCCTTTGATGCGACCCAGTCCAGTGTG 532
 QY 524 CACTGTTTCAATGGAAGAACTATATCTGAGCCACAGATGATGATGATGATGATGATGAT 583
 Db 533 CCATCTCTGACAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 592
 QY 584 CAGTCATTTACGGAAGTCTGAGAGAAAGCCCTACCTGCGGAGCCGTCAAGCAGATTCAA 643

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Db 593 CTGTGTTTACAGAGCCTTGACCTGACGCCCTCCGTTCTGCAAAAGTATGACTCA 652
QY 644 AATGTTGAAAGACACTTCTTGACGCGGTGATTAACGAGATTATATCTACTCT 703
Db 653 AGTGGCTCGAGACCCACACTTTCTATGCTTGAGCATGAGACCATCTACTACTCT 712
QY 704 TCTTCAGGAAATAGCAGTGAATATA--ACACCATGGGAAAGTATTTCCCAAGAG 760
Db 713 TTCTCCGAGAAAGTCTCTGTGGAGGAGCGCCGCGGAGGAGGAGTTCAGTTTCCGGG 772
QY 761 TGGCTCAGGTTTGAAGATATGATGGAGAGATCTCAAGAGTCTGAGAGAAACATGGA 820
Db 773 TGGCCCGGAGTGTGAAGCTGACATGGGTGCTCACCAGCGGCTTGATGCCACATGGA 832
QY 821 CGTGTTCCTGAGAGCGGCTTGAAGTCTGAGTCTGAGTCTGAGACTCTCATTTTATTTCA 880
Db 833 CATCTTCCTTAAGCTGAGGCTCAAGTCTGCTCCGCGGAGGAGTCACTTCTTACTTTG 892
QY 881 ACATTTCAGGAGCTTACAGATGATGATGCTATCAACGCGGCGTGAATGTTGCTCCGCAA 940
Db 893 ATGCTTACAGTCTTAACTGAGGCTTGAACTGCAATGGGCGCTCTGCTCTTTGGGG 952
QY 941 CGTTTCTACACTTAAACAGACATCCCTGGGCTGAGCTGTGCTATGACATGCTTG 1000
Db 953 TCTTACTACTCAAGACCATAGCATCTCTGGGCTGCGAGTCTGGGCTTCTACTAGATG 1012
QY 1001 ACATTGCCAGTGTTTTACTGAGGAGATTCAGAGAAAGAACTCTCTGATTTCCACTGGA 1060
Db 1013 ACATTGAAGCTGTGTGAGGAGCAAGTTCAGAGGAGCAAGTCTGATGGGCGTGA 1072
QY 1061 CACCACTTCCTGATGAGACGATTCCTAGCCAGGCGCGAGTGGCTGCTGGCTCATCT 1120
Db 1073 CTCTGTCTGAGAGCAAAAGTCCCTCACCAGGCGAGGCTGCTGCTGAGGCTG 1132
QY 1121 CCTTGAAGATATGCAACTCCATCAATGAGTCCCTGATGATACCTGATTCATCAAGA 1180
Db 1133 CAGCTGCTTATCTCTCTCTCTCTCAAGACCTGCTGAGAGATGCTGCTCTTCAACAAG 1192
QY 1181 GCGACCGGCTCATGATGAGGAGTGGCTCCATCTTCAACAGGCGCATGCTCTGAGAA 1240
Db 1193 CACACCGACCTGCTGATCCGCTGCTGAGCACC--TGCCACCCATCAACCTCTCCCTC 1249
QY 1241 CAATGCTGAGATACCGCTTACCAAAATTCAGATGAGGAGACAGCTCTGGGCGCATGGA 1300
Db 1250 TGACTAGAGGCTCTACTGACCCAGTACGTGTGATGCTGAGCTGAGCCGCCAGAA 1309
QY 1301 ATCACACTGTGTTTCTTGAGATCAGAGAAAGGAAATCATCTTGAAGTTTGGCCAGAA 1360
Db 1310 ATACTACAGTCTCTGTTGCTGCTCAATGATGAGGACAGTCTGAAAGGTGACTACCTCAG 1369
QY 1361 TAGAAGATAGTGTCTTAATATGACAGCTTTCTCGAGAGAGATGATGTTTACACT 1420
Db 1370 GGGGACA--GTCTGTGGAGACCCGAGCCATCATTTGGAAGATGATGATGCTCAGAGC 1426
QY 1421 CTTGAAAAATGACGATATGATG--AGTGAAGACAAAAGATCATGGGCTGACAGC 1474
Db 1427 ATGCCCCGTGAGTGGAGAGCGGTACCCCGAGCTGCTGACGAGATCATAGGCGTGAAC 1486
QY 1475 TGGAGAGAGCAAGCACTCTGTATGTTGCGTTCTTCACTGTGTATAAAGTTCCCC 1534
Db 1487 TGGACACGAGGAGTACAGAGCTTTTGGGCTTTCCTGATGACATCGTCACTCTC 1546
QY 1535 TTGGCCGGTGTAGAGGACATGGGAAGTGTAAAAAACCTGTATGCTCTCAAGAGCCAT 1594
Db 1547 TTAGCGCGCTGCTCCCGGAGTGAAGCATGTCAAGAGAGGCTGCTGCTTCTGAGACCAT 1606
QY 1595 ATTGTGATGG 1605
Db 1607 ACTGTGATGG 1617

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RESULT 6
US-09-254-594-1

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: Sequence 1, Application US/09254594
: Patent No. 6566094
: GENERAL INFORMATION:
: APPLICANT: KIMCHI, Toru
: APPLICANT: KIMCHI, Kaoru
: TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
: FILE REFERENCE: 0020-4527P
: CURRENT APPLICATION NUMBER: US/09/254,594
: CURRENT FILING DATE: 1999-05-11
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 1
: LENGTH: 3195
: TYPE: DNA
: ORGANISM: Rattus norvegicus
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(3195)
: OTHER INFORMATION: Tissue Type: Brain
: NAME/KEY: 5'UTR
: LOCATION: (1)..(50)
: OTHER INFORMATION: Identification Method: E
: NAME/KEY: misc_feature
: LOCATION: (51)..(2837)
: OTHER INFORMATION: CDS; Identification Method: E
: NAME/KEY: 3'UTR
: LOCATION: (2838)..(3195)
: OTHER INFORMATION: Identification Method: E
: US-09-254-594-1

Query Match 12.0%; Score 369.8; DB 4; Length 3195;
Best Local Similarity 55.9%; Pred. No. 5,4e-89;
Matches 811; Conservative 0; Mismatches 622; Indels 18; Gaps 5;

QY 164 GCGTGGACATCCAGATGATATGATCATGAAACGAAACCTCTACTTCTGCTAGGAGC 223
Db 226 GCGTGGACATTCAGAGATTCCTGACCTTGAACCGGAGCCTTGTGTGCTGCGGAGC 285
QY 224 ATATTATATCTGTATATATGACATCATCAACAGGAAATTTATGTAGCAAAAAC 283
Db 286 AGCTTTTCTCTGATCTTCAAGCCCAAGAAAGAGGAGGCTGCTGCCAACAAAT 345
QY 284 TGACATGGAATCTAGACAGGCGGATGTAGACATGACAGATGAGAGGAAACATTAAG 343
Db 346 T---TCTGACATGGGAGGAGCCAGACATGAGAAATGTCTCCGGGAGAGCTGACGG 402
QY 344 ATGATGCCCAACTTTATTAAGTTCTTCTTAAGAAAAACCATGATGATTTGTGCT 403
Db 403 ACGAATGCTACAACTACATCCGTTCTTCTTCCCTGGGACTGCGAGATCTCTGCT 462
QY 404 GTGGAACTATGCTTCAACCTTCTCTGAGAACTATPAGATGATATGATGAAACAT 463
Db 463 GTGGAACTATGCTTCAACCTTCTCTGAGAACTATPAGATGATGATGATGAAACAT 522
QY 464 TCGGGAGTGAATTCAGCGGAGATGCGGAGATGCCATGATGATGCCAATGCCAGCTG 523
Db 522 AGGGTGAAGAGCTGATGAGGAGCTGATGAGCTGATGAGCTGATGAGCTGATGAG 582
QY 524 CACTGTTTGAATGGAATATGATGATGATGATGATGATGATGATGATGATGATGATG 583
Db 583 CCATCTCTGCAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 642
QY 584 CAGTCAATTAACGAGATCTTGAAGAAAGCCCTACCTGCGGAGCCGTCAGCAAGATCAA 643
Db 643 CTGTGTTTACAGAAAGCCCTTGAAGCCCTACGACCCCACTCTGTCGAAAGATGATCA 702
QY 644 AATGTTGAAGAACATCTTTGTTCAAGCCGCTGATATGAGAGATATATCTACTCT 703
Db 703 AGTGGCTTGAAGAGCCACATTTTGTATGCTTTGAGAGATGAGAGCCATGCTACTCT 762
QY 704 TCTTCAGGAAATAGCAGTGAATATA--ACACCATGGGAAAGTATTTCCCAAGAG 760
Db 763 TTCTCCGAGAAAGTCTCTGTGGAGGAGCGCCGCGGAGGAGGAGTTCAGTTTCCGGG 822

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QY 761 TGGCTCAGGTTGGTAAAGATATATGAGGAGATCTCAAGAGAGCTGGAGAACAGTGA 820
 DB 823 TGGCCCGGGGTGTAAACGTGACATGAGGAGGCTCACACGAGGCGCTGGATCGCACGGA 882
 QY 821 CGTGTCTCCGAAGGCGCGTGAAGTCACTGCTCACTCTCTGAGAGCTGCTATTATTTCA 880
 DB 883 CATCTCTCTTAAGCTGAGGCTCACTGCTCGCTCCCTGGAGACTGCTACTCTTACTTTG 942
 QY 881 ACATTCTCCAGGAGATTACAGATGTATTCATCAAGGCGCTGATGTTGCTCTGCA 940
 DB 943 ATGTCTTACAGTCTTAACTAGGCGCTGTGAACCTGTGATGGCGCTCTGCGCTTTGGGG 1002
 QY 941 CGTTTCTACACTTAAACAGATCCCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1000
 DB 1003 TCTTCACTACTCAACCAATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1062
 QY 1001 ACATTGCAAGTCTTTTACTGAGGATTCAGAGAGAGAGTCTGCTGATTCACCTGGA 1060
 DB 1063 ACATTGAGGCTGCTTTGAGGAGAGATTCAGAGAGAGAGTCTGATGGAGGCGCTGGA 1122
 QY 1061 CACCAAGTCTCTGATGAACAGTCTTAAGCCGAGGCTGCTGCTGCTGCTGCTGCTGCT 1120
 DB 1123 CTCTGTGTCTGAGGACAAAGTCCCTCACCCAGGCGAGGCTGCTGCTGCTGCTGCTG 1182
 QY 1121 CCTTAAAGATATGACACCTCAATGAGTTCCTGATGATGATGATGATGATGATGATG 1180
 DB 1183 CAGCTGCTTATCTCTCTCTCTCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1242
 QY 1181 CGACCCCGCTCATGATGAGGAGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1240
 DB 1243 CACACCCAGTGTGATCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1299
 QY 1241 CAATGCTCATATACCGCTTACCAAAATTCAGTGGAGCAAGCTGCTGCTGCTGCTGCTG 1300
 DB 1300 TGACTGACGAGGCTCTACTGATGACCCAGTACTGCTGATGCTGCTGCTGCTGCTG 1359
 QY 1301 ATACACCTGCTGCTTTTCTGAGATTCAGAGAGAGAGATTCATCTTGAATTTTGGCCG 1360
 DB 1360 ATACTACAGTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1419
 QY 1361 TAGGAATAGTGTCTTCTTAATGACAGCTTTTCTGAGAGAGATGATGTTTACACT 1420
 DB 1420 GGGGACA--GTCCTCTGAGACCCGAGGCTTCAATATGAGAGATGATGCTGCTG 1476
 QY 1421 CTGAAGAAATGACAGTATGATG--AGTGAAGAGAAAGATATGAGATGAGATGAGC 1474
 DB 1477 ATGCGCGGTGAGGAGAGCGGTCACCCGAGCTGCTGAGAGATATAGGCTGAGC 1536
 QY 1475 TGGACAGAGCAAGCAGCTCTGTATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1534
 DB 1537 TGGACACTGAGGAGTACAGGCTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1596
 QY 1535 TTGGCGGCTGAGAGAGATGAGAGAGTGAAGAAACCTGATGCTGCTGCTGCTGCTG 1594
 DB 1597 TCACCCGCTGTGCGCGGATGAGAGATGACAGAGAGTGTGCTGCTGCTGCTGCTG 1656
 QY 1595 ATTGTGATG 1605
 DB 1657 ACTGTGATG 1657

RESULT 7
 US-08-121-713D-57
 : Sequence 517, Application US/08121713D
 : Patent No. 5639856
 : GENERAL INFORMATION:
 : APPLICANT: Goodman, Corey S.
 : APPLICANT: Kolodkin, Alex L.
 : APPLICANT: Mathes, David
 : APPLICANT: Bentley, David R.
 : APPLICANT: O'Connor, Timothy
 : TITLE OF INVENTION: The Semaphorin Gene Family

: NUMBER OF SEQUENCES: 100
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: SCIENCE & TECHNOLOGY IAW GROUP
 : STREET: 268 Bush Street, Suite 3200
 : CITY: San Francisco
 : STATE: CA
 : COUNTRY: USA
 : ZIP: 94104
 : COMPUTER READABLE FORM:
 : MEDIM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/121,713D
 : FILING DATE: 13-SEP-1993
 : CLASSIFICATION: 514
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Osman, Richard A.
 : REGISTRATION NUMBER: 36,627
 : REFERENCE/DOCKET NUMBER: B94-002-1
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (415) 343-4341
 : TELEFAX: (415) 343-4342
 : TELEX:
 : INFORMATION FOR SEQ ID NO: 57:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 2854 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: double
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: 451..2640
 : US-08-121-713D-57
 : Query Match 5.4%; Score 166; DB 1; Length 2854;
 : Best Local Similarity 53.0%; Pred. No. 2,2e-34;
 : Matches 532; Conservative 0; Mismatches 415; Indels 57; Gaps 6;

QY 289 TGGAAATCTAGACAGGCGGATGTGACACATGACAGATGAGGAGAAACATTAAGATGAG 348
 DB 709 TGGCAGCTGTCAGGCTGACGACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 768
 QY 349 TGGCAGCACTTATTAAAGTCTCTTAAGAAACGATGATGCTGCTGCTGCTGCTGCTG 408
 DB 769 TGGCAGAACTTACATCCGAGTCTGCGCAAAATGACATGACCGGATCTGCTGCTG 828
 QY 409 ACTAATGCTTCAACCTCTCTGCAAGAACTATAGAT--GATATATTGGAACATTC 465
 DB 829 ACGAAGCCCTATAGAGCCACTATGTGCGCACTACGCGCTCAAGAGATGAGATGATG 888
 QY 466 GGGGATGATCTACCGGAGATGCGCAAGTGCCTATGATGCAACATGCGCAAGTTGCA 525
 DB 889 GAGAAATATATGAGGAGAGAGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 948
 QY 526 CTGTTGCAATGAGAAACATTAATCTGACGCAAGTGAAGTCTGCTGCTGCTGCTGCTG 585
 DB 949 ATATACAGTGTGAGGAGACATTTACTACGCAACAGTGGGAGACTTCTGTGGAACAG 1008
 QY 586 GTCAATTACCGGAGTCTTGGAGAAAGCCCTACCTGCGGAGCCGTCAACAGCATTCAAA 645
 DB 1009 CTCAATATACCGCGCC-----CTTAAGAACAGAGATCTGACCTCAAA 1053
 QY 646 TGGTTGAAGACATATGTTGTCAGAGCCGCTGATGACGAGATTAATCTACTTCTTC 705
 DB 1054 CAATTAAATGCTCTTAATCTTGTGACAGCATGAGATGATTAATTAATCTCTTC 1113
 QY 706 TTCAGGAAATAGAGAGTGTGATTAACCATGGAAGGATGTTTCCCAAGAGTGTCT 765
 DB 1114 TTCGAGAGAGTGTGTGATGATCAATGCGGAAAGGCTATCTATTCAGAGTGTCC 1173

Db	1471	AACGCGTTGGCAGTGGCCAAAGCCTTAAAGTGGCAGAACCAAGGCGCTGCACAAATGCT----	1526
QY	1114	TCATCTCTCTTAGAAGAGATATGCAACCTCCAAATGATTCCTATGATACCTTAACCTC	1173
Db	1527	-----GAAATGACAGTCTGTACAC-----TTCTGTATGTGTCTGTCAAAATTT	1566
QY	1174	ATCAAGAGCGACCCGGCTCATGAGATGAGAGCAGTGGCCCTCCATCTTCACAAAGGCCAATGGTTC	1233
Db	1567	GTAAGTGCACATATACATGATGATGAGAGAGCGGTGCAGCAATTTTCTACTCGGCCAATTCTC	1628
QY	1234	CTGAGAACAAATGTCATAGATACCGGCTTACCAAAAATTTGCAGTGGGA	1277
Db	1627	ATTGGGATCAGCCTTACAGTACAGATTAACAAAATTAACCTGTGGA	1670

RESULT 9
US-09-060-692-57
; Sequence 57, Application US/09060692

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1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: Floppy disk
3  COMPUTER: IBM PC compatible
4  OPERATING SYSTEM: PC-DOS/MS-DOS
5  SOFTWARE: PatentIn Release #1.0, Version #1.25
6  CURRENT APPLICATION DATA:
7  APPLICATION NUMBER: US/09/060,692
8  FILING DATE:
9

```

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1      FILING DATE: 13-SEP-1993
2      ATTORNEY/AGENT INFORMATION:
3      NAME: Osman, Richard A.
4      REGISTRATION NUMBER: 36,627
5      REFERENCE/DOCKET NUMBER: B94-002-1
6      TELECOMMUNICATION INFORMATION:
7      TELEPHONE: (415)343-4341
8      TELEFAX: (415) 343-4342
9      TELEX:
10     INFORMATION FOR SEQ ID NO: 57:
11     SEQUENCE CHARACTERISTICS:
12     LENGTH: 2854 base pairs
13     TYPE: nucleic acid
14     STRANDEDNESS: double
15     TOPOLOGY: linear
16     MOLECULE TYPE: cDNA
17     FEATURE:
18     NAME/KEY: CDS
19     LOCATION: 451..2640
20     US-09-060-692-57

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QY	343	TGGCAACACTTATTTAAAGTCTCTTAAAGAAAAAGATGATCATTTGTTGCTGTGA	408
Db	769	TGGCAAACTACTATCCGAGTCCCTGGCGAAATTTGAGATGACCGGTACTCACTTCGGGT	828
QY	409	ACATATGCGCTTCAACCTTCTCTGACAAACTATATAGAT---GGATCAATTGGAAACCATTC	465
Db	829	ACGACAGCCCTATAGGCACACTATGTGGCACTACGCCCTCAAGATGAGATATATGTTGTA	888
QY	466	GGGGATGAATTCAGCGGAATGSCCAAGTCCCATATGATGCCAAACATGSCAACGTTCGA	525
Db	889	GAGAAAAGAAATATGAGGGAAGAGGATTTGTGCCATTTTGACCTGACCAACACACACTGCA	948
QY	526	CTGTTTGCAATGAAAAACATATACCTAGACACAGTGCCTACTTCTCTGCTATGACGCA	585
Db	949	ATATACAGTAGGGACATTTGTATCTACGCAACAGTGCAGACTCTCTGTGGAACTGACCT	1008
QY	586	GTCATTTACCGGAGCTCTGGAGAAAAGCCCTACCCCTGGGACCGTCAAGACGATTCAAA	645
Db	1009	CTCATATACCGGGCC-----CTCTAAGAACAGAGATCTGACCTTCAAA	1053
QY	646	TGCTTGAAGACCATTACTTTGTTCAAGCGCTGATATCGAGATTTATCTCTCTTC	705
Db	1054	CAATTAATCTCTCTACTTTGTCACACAAATGAGATCAATGATTTATATCTCTTCTTC	1113
QY	706	TTTCGGGAAATAGACAGTGGAGTATACACCATGGGAAGGTAGTTTCCCAAGAGTGGCT	765
Db	1114	TTTCGAGAGACTGCTGTGTTGAGTACATACACTGGGGAAGGCTACTCTTTCAGAGTGGCC	1173
QY	766	CAGCTTTGTAGAAATGATATGGAGAGATCTCAAAAGTCCCTGGAGAAACAGTGCAGCTG	825
Db	1174	AGAGCTGTGTAATACATGACAAAGGCGGCGCCCTCATAGGGTGGTGAACA---TGGACCTCT	1230
QY	826	TTTCTGAAGGGCGCTTGAACCTGCTCAGTCCCTGAGACCTCATTTTATTTTACCATY	885
Db	1231	TTTTTGAATACCTCTGAACTGTTCGCTCCCTGAGATTAATTCATTTTACTTTAAATGA	1290
QY	886	CTTCAGGCAAGTACAGATGATTCGATACGACGCGGCTGATATGTTGTCCTGGCAAC---	941
Db	1291	ATTACATCAACAAATGACATCATTTGAAGGAATATATGTTGTCAAATGGAACAACTATC	1350
QY	942	-----GTTTCTTACACTTATPACAGCATCCCTGGGTGTCGAGTCTGTCCTATGAC	993
Db	1351	TACGGTGTCTACAGACACACAGTAACTCTATGTTGGTGGCTCTGCTGTGTTGCCCTTCA	1410
QY	994	ATGCTTGACATTTGCCAGTGTTTTACTGTGGAGATTTCAAGGAACGAAGATCTGCTGATCC	1053
Db	1411	ATGAAAGTCAAATCTTGACTCATTTGATGAGTGCATTTTAAAGGCGAGABACATGAACTCA	1470
QY	1054	ACMGAGACACAGCTCTGATGAACGAGTTCCTTAAGCCACGAGCCAGTTGCTGTGTCGC	1113
Db	1471	AACGTGTTGGCAGTCCCAAGCCTTAAATGTGCAGAACCAAGGCGCTGGACATATGT---	1526
QY	1114	TCATCTCTTAGAAGATATGCAACCTCCAAATGATGTTCCCTGATGATACCTTGAACTTC	1173
Db	1527	-----GAATGACAGTCGTACAC-----TTCTGATGTTGTCGTCAATTTT	1566
QY	1174	ATCAAGACGACCCGCTCATGATGATGAGCAAGTGCCTCATCTTCAACAGGCAATGTTTC	1233
Db	1567	GTTAAAGTCACATACCTGATGATGATGAGGCGCGTGCACGATTTTTTTACTCGGGCAATTTCTC	1622
QY	1234	CTGAGAACAAATGTCAGATATCGGCTTTACCAAAATTTGACATGGA	1277
Db	1627	ATTGGATACGCTTACAGTACGATATCAAAAAATAGCTGTGA	1670

RESULT 10
US-08-833-391-57
; Sequence 57, Application US/08833391
; Patent No. 6013781
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.

Db 407 GCCTGGCCGCGCTGCAATGAGGACAAAGTGCGCCGATCATTC--GCACCGCT 463
 QY 818 GGAGCTGCTCTGGAAGGCGGCTTGAAGCTGCTGCTGCTGAGACTCTATTATT 877
 Db 464 GGACATCTCTCCCAAGTCCGCTCAACGCTCAATCCCGGATTAACCTTTTACT 523
 QY 878 TCAACATCTCCAGGAGTATGATGATGAT-----TCGATCAAGGGGCTG 925
 Db 524 TTAATGAATCAATCTGCCAGCAATCTGTTGAGAGGAGACGATGCTCATGACG 583
 QY 926 ATGTGCTGCTGCAAGCTTTTCTACACCTTATACAGCATCCCTGGCTGACGCTG 985
 Db 584 AACTGATCTAGGAGTCTTCAACACGCGAGCAACTCATCCCGGCTGACGGTTGTG 643
 QY 986 CCTATGACATGCTTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1045
 Db 644 CCTTGGCCCTCCAGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 703
 QY 1046 CTGATTCACCTGAGACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1105
 Db 704 TCACTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 763
 QY 1106 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1165
 Db 764 GTCAACAGATTCG-----AGAGGCTTCCGGATCCGACAC 799
 QY 1166 TGAATCTCATCAGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1225
 Db 800 TGAATCTCATCAGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 859
 QY 1226 CAGTCTCTGAGACAAATGCTGAGATCCGCTTACCAAAATGCAAGTGA 1277
 Db 860 CGATTCTGCTGAGACAAATGCTGAGATCCGCTTACCAAAATGCAAGTGA 911

RESULT 14

US-08-835-268-59
 : Sequence 59, Application US/08835268

Patent No. 5807826

GENERAL INFORMATION:

: APPLICANT: Goodman, Corey S.
 : APPLICANT: Kolodkin, Alex L.
 : APPLICANT: Mathes, David
 : APPLICANT: Bentley, David R.
 : APPLICANT: O'Connor, Timothy
 : TITLE OF INVENTION: The Semaphorin Gene Family
 : NUMBER OF SEQUENCES: 100
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 : STREET: 268 Bush Street, Suite 3200
 : CITY: San Francisco
 : STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/835, 268

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/121, 713

FILING DATE: 13-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: Osman, Richard A.

REGISTRATION NUMBER: 36, 627

REFERENCE/DOCKET NUMBER: B94-002-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415)343-4341

: TELEFAX: (415) 343-4342
 : TELETYPE:
 : INFORMATION FOR SEQ ID NO: 59:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 3560 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: double
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: 1..1953
 : US-08-835-268-59
 Query Match 4.7%; Score 146.4; DB 1; Length 3560;
 Best Local Similarity 51.9%; Pred. No. 4.4e-29;
 Matches 494; Conservative 0; Mismatches 401; Indels 57; Gaps 5;

QY 341 AGATGAGTGGCCACACCTTATTAAAGTTCTTTAAAGAAAACGATGATGCTTTG 400
 Db 2 AGATGAGTGGCCACACCTTATTAAAGTTCTTTAAAGAAAACGATGATGCTTTG 61
 QY 401 TCTGTGAGACTAATGCTTCACCTTCCTGACAAACTATTAAGAT--GGATCAATGG 457
 Db 62 TTTGTGCAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 121
 QY 458 AACCATTCGGGATGAAATTCAGCGAAATGGCCAGATGCCATATATGACCAATGCCA 517
 Db 122 AACCATTCGGGATGAAATTCAGCGAAATGGCCAGATGCCATATATGACCAATGCCA 181
 QY 518 ACCTTGCAGCTGTTGCAAGATGAAATACATACAGCAGCAGTACATGCTTCTGCA 577
 Db 182 CCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 241
 QY 578 TTGACGAGCTATTACCGGAGTCTTGGAGAAACCTTACCTGCGGACGCTGACGACG 637
 Db 242 GCGATCCGATTATCTACCGGAGC-----CCCTGACAGCCGACGATGACG 286
 QY 638 ATTCAAAATGCTTGAAGAACCACTTGTTCACGCGGTGATTCGAGATTAATCT 697
 Db 287 ATTCAAAATGCTTGAAGAACCACTTGTTCACGCGGTGATTCGAGATTAATCT 346
 QY 698 ACTTCTTCTTGAAGAAATACAGTGGATTAACACCATGGGAAAGTATGTTCCCAA 757
 Db 347 ATTCTCTTCTTGAAGAAATACAGTGGATTAACACCATGGGAAAGTATGTTCCCAA 406
 QY 758 GAGTGGCTCAGCTTGTGAAGATGATGAGAGATCTCAAGAGTCTGAGAGAAACAGT 817
 Db 407 GCGTTGCCCGCTGCAAAATGGAGCAAAAGTGGCCCGCATGATGCTC--GCAACGCT 463
 QY 818 GGAGCTGCTTCTGAAAGCGGCTTGAACCTGCTAGTTCCTGAGAGCTCTCATTTTAT 877
 Db 464 GGAGCTGCTTCTGAAAGCGGCTTGAACCTGCTAGTTCCTGAGAGCTCTCATTTTAT 523
 QY 878 TCAACATCTCCAGGAGTATGATGATGAT-----TCGATCAAGGGGCTG 925
 Db 524 TTAATGAATCAATCTGCCAGCAATCTGTTGAGAGGAGACAGATGCTCATGACG 583
 QY 926 ATGTGCTGCTGCAAGCTTTTCTACACCTTATACAGCATCCCTGGCTGACGCTG 985
 Db 584 AACTGATCTAGGAGTCTTCAACAGCGGAGCAACTCAATCCCGGCTGACGGTTGTG 643
 QY 986 CCTATGACATGCTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1045
 Db 644 CCTTGGCCCTCCAGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 703
 QY 1046 CTGATTCACCTGAGACAGTTCCTGATGAGAGCTTCTAAGCCAGGCGCAAGTGTCT 1105
 Db 704 TCACTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 763
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 Db 764 GTCAACAGATTCG-----AGACGCTTCCGATCCGACAC 799

QY 1166 TGAATTCATCAGAGCAGCCGCTCATGATGAGGAGTCCCTCATCTTCAACAGGC 1225
 |||||
 Db 800 TGAATTCATCAGAGCAGCCGCTCATGATGAGGAGTCCCTCATCTTCAACAGGC 859
 QY 1226 CATGTTCTCTGAGAACATGCTCAGATACCGCTTACCAAAATTGCAGTGA 1277
 |||||
 Db 860 CGATTTTGGTCCGAGCAGACAAATATACCGCTTCACTCAAAATCCCGCTAGA 911

RESULT 15

US-09-060-692-59
 ; Sequence 59, Application US/09060692
 ; Patent No. 5935865

GENERAL INFORMATION:

APPLICANT: Goodman, Corey S.
 APPLICANT: Kolodkin, Alex L.
 APPLICANT: Mathes, David
 APPLICANT: Bentley, David R.
 APPLICANT: O'Connor, Timothy
 TITLE OF INVENTION: The Semaphorin Gene Family
 NUMBER OF SEQUENCES: 100
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 STREET: 268 Bush Street, Suite 3200
 CITY: San Francisco
 STATE: CA

COUNTRY: USA
 ZIP: 94104

COMPUTER READABLE FORM:

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 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/060,692

FILING DATE:

CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/121,713

FILING DATE:

ATTORNEY/AGENT INFORMATION:
 NAME: Osman, Richard A.

REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: B94-002-1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415)343-4341

TELEFAX: (415) 343-4342

TELEX:
 INFORMATION FOR SEQ ID NO: 59:

SEQUENCE CHARACTERISTICS:
 LENGTH: 3560 base pairs

TYPE: nucleic acid
 STRANDEDNESS: double

TOPOLOGY: linear
 MOLECULE TYPE: CDNA

FEATURE:
 NAME/KEY: CDS

LOCATION: 1..1953
 US-09-060-692-59

Query Match 4.7%; Score 146.4; DB 2; Length 3560;
 Best Local Similarity 51.9%; Pred. No. 4,4e-29;
 Matches 494; Conservative 0; Mismatches 401; Indels 57; Gaps 5;

QY 341 AGGATGAGTGCACAACTTATTAAGTCTCTTAAGAAAAAGCATGATGATGTTG 400
 |||||
 Db 2 AGGATGAGTGCACAACTTATTAAGTCTCTTAAGAAAAAGCATGATGATGTTG 61
 QY 401 TCTGTGAACTAAAGCTTCAACCTTCCTGCAAGAACTATAGAT---GGATACATGG 457
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 Db 62 TTTGTGGCACCACATCTGTTCCGGCCCATGTGCACACAGCTATATCATTAAGTACAGCACT 121

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Search completed: September 30, 2003, 22:06:04
 Job time: 216.509 secs

OM nucleic - nucleic search, using sw model

10107.639 Million cell updates/sec

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Scoring table: IDENTITY_NUC
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Total number of hits satisfying chosen parameters: 3357240

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Post-processing:	Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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2	3038	99.2	3498	11	US-09-957-187-3	Sequence 3, Appl1
3	3030.4	99.0	4250	11	US-09-957-187-84	Sequence 84, Appl1
4	2698	87.2	3333	11	US-09-991-053-5	Sequence 5, Appl1
5	2698	87.2	3333	11	US-09-957-187-5	Sequence 5, Appl1
6	1881.6	60.8	1890	11	US-09-991-053-29	Sequence 29, Appl1
7	1881.6	60.8	1890	11	US-09-957-187-82	Sequence 29, Appl1
8	1881.6	60.8	1890	11	US-09-957-187-82	Sequence 82, Appl1
c	604	18.5	846	10	US-09-833-381-920	Sequence 920, App
10	565	18.3	1472	9	US-09-925-299-60	Sequence 60, Appl1
11	565	18.3	1472	11	US-09-925-299-60	Sequence 60, Appl1
12	555.4	17.0	3524	12	US-10-391-413-3	Sequence 3, Appl1
13	553.8	18.0	3721	11	US-09-931-836-34	Sequence 34, Appl1
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16	553.8	17.9	3721	12	US-10-140-016-543	Sequence 543, App

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45	553.8	17.9	3721	12	US-10-147-495-543	Sequence 543, App

ALIGNMENTS

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RESULT 1
US-09-991-053-3
Sequence 3, Application US/09991053
Publication No. US20030003532A1
GENERAL INFORMATION:
APPLICANT: Shinketsu, Richard A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES ENCODING HUMAN
TITLE OF INVENTION: MEGF-, AND ROUNDABOUT-LIKE POLYPEPTIDES
FILE REFERENCE: 15966-540 CON S-1-10
CURRENT APPLICATION NUMBER: US/09/991, 053
CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: USSN 60/123,667
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: 09/520,781
PRIOR FILING DATE: 2000-03-08
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 3498
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (214)..(3030)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (3047)
OTHER INFORMATION: an n may be any one of a or t or g or c
US-09-991-053-3

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Best Local Similarity	99.3%	Pred. No. 0;		
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; Publication No. US2003005451A1			
; GENERAL INFORMATION:			
; APPLICANT: Shimkets, Richard A.			
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY			
; FILE REFERENCE: 15966-540 CIP			
; CURRENT APPLICATION NUMBER: US/09/957,187			
; CURRENT FILING DATE: 2000-09-19			
; PRIOR APPLICATION NUMBER: 60/123,667			
; PRIOR FILING DATE: 1999-03-09			
; PRIOR APPLICATION NUMBER: 09/520,781			
; PRIOR FILING DATE: 2000-03-03			

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Prior	FILING DATE:	2000-09-20
Prior	APPLICATION NUMBER:	60/233,798
Prior	FILING DATE:	2000-09-19
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Prior	FILING DATE:	2000-01-04
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FEATURES:		
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LOCATION:	(214)..(3030)	
NAME/KEY:	misc_feature	
LOCATION:	(3047)	
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Db	454	ATGACACATCCACACGGAAGAAATTTATTGTAGCAAAAAAAGTACATGGAAATCTAGA 513
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OY	361	ATTAAAGTCTTCTAAGAAAAAGCATGTGCAATGTTGTCTGTGGAACTAATGCTTTC 420
Db	574	ATTAAAGTCTTCTAAGAAAAAGCATGTGCAATGTTGTCTGTGGAACTAATGCTTTC 633
OY	421	AACCTTCTCTGCAAGAACTATAAGATGGATTAATTTGAAACCAATTCGGGGATGAATTCAC 480
Db	634	AACCTTCTCTGCAAGAACTATAAGATGGATTAATTTGAAACCAATTCGGGGATGAATTCAC 693
OY	481	GGAATGCCAGATGGCCCATATGATGSCAAACATGCCAACGTTGCACTGTTTGCAGATGA 540
Db	694	GGAATGCCAGATGGCCCATATGATGSCAAACATGCCAACGTTGCACTGTTTGCAGATGA 753
OY	541	AAACTATACACGCCACAGTAGTACTCTTCCTGCAATGAGCGCACTCAATTAACCGAGT 600
Db	754	AAACTATACACGCCACAGTAGTACTCTTCCTGCAATGAGCGCACTCAATTAACCGAGT 813
OY	601	CTTGAGAAAGCCCTACCTCGCGGACCGTCAAGCAGATTCAAATATGTTGAAAGAACCA 660
Db	814	CTTGAGAAAGCCCTACCTCGCGGACCGTCAAGCAGATTCAAATATGTTGAAAGAACCA 873
OY	661	TACTTTGTTCAAGCCGTGATTCACGAGATTTATATCTACTCTTCTTCAGGGAAATAGCA 720
Db	874	TACTTTGTTCAAGCCGTGATTCACGAGATTTATATCTACTCTTCTTCAGGGAAATAGCA 933
OY	721	GTCGAGATTAACACATGGGAAGGATGTTTTCCCAGAGGTGCTCAGGTTTGTAAAGAT 780

Db	934	GTGAGATATACACCATGGGAAGTAGTTTCCCAAGATGGCTCAGTTTGTAAAGAT	993	
Qy	781	GATATGGAGGATCTCAAGAGTCTGGGAAGACATGGACGTGTTCCGAAGGGCGC	840	
Db	994	GATATGGAGGATCTCAAGAGTCTGGGAAGACATGGACGTGTTCCGAAGGGCGC	1053	
Qy	841	TTGACGTGCTCAGTTCCTGGAGACTCTCATTTTATTTTCAACATTCCTCCAGGAGTTTACA	900	
Db	1054	TTGACGTGCTCAGTTCCTGGAGACTCTCATTTTATTTTCAACATTCCTCCAGGAGTTTACA	1113	
Qy	901	GATGTGATTCGATCAACGGGGGTGATGTTGCTCGGCAACGTTTCTTACACTTATAC	960	
Db	1114	GATGTGATTCGATCAACGGGGGTGATGTTGCTCGGCAACGTTTCTTACACTTATAC	1173	
Qy	961	AGGATCCCTGGGTCTGAGCTGTGCTATGACATGTTGACATGGCAGTGTATTTACT	1020	
Db	1174	AGGATCCCTGGGTCTGAGCTGTGCTATGACATGTTGACATGGCAGTGTATTTACT	1233	
Qy	1021	GGGAGATTCAGGAGACGAAGTCTCTGATTTCCACTGGACACCACTTCTGTATGAACGA	1080	
Db	1234	GGGAGATTCAGGAGACGAAGTCTCTGATTTCCACTGGACACCACTTCTGTATGAACGA	1293	
Qy	1081	GTTCTTAAGCCGACGAGTGTGCTGTGCTGCTCATCTCTTAAAGAAATATGCAACC	1140	
Db	1294	GTTCTTAAGCCGACGAGTGTGCTGTGCTGCTCATCTCTTAAAGAAATATGCAACC	1353	
Qy	1141	TCCAAATGATTCCTCTGATGATACCTTCATCAGACGACCCGCTCATGATGATG	1200	
Db	1354	TCCAAATGATTCCTCTGATGATACCTTCATCAGACGACCCGCTCATGATGATG	1413	
Qy	1201	GCAAGTCCCTTCATCTTCAACAGGCCATGTTCTCTGAAACAAATGTCAGATACCCCTT	1260	
Db	1414	GCAAGTCCCTTCATCTTCAACAGGCCATGTTCTCTGAAACAAATGTCAGATACCCCTT	1473	
Qy	1261	ACCAAAATGCAATGGAGACAGGCTGCTGGGCCATATGCAATCACTGATGTTTCTG	1320	
Db	1474	ACCAAAATGCAATGGAGACAGGCTGCTGGGCCATATGCAATCACTGATGTTTCTG	1533	
Qy	1321	GGATCAGAGAGGGAATCATCTTGAAGTTTTTGGCCAGAAATAGAAATAGTGTGTTCTA	1380	
Db	1534	GGATCAGAGAGGGAATCATCTTGAAGTTTTTGGCCAGAAATAGAAATAGTGTGTTCTA	1593	
Qy	1381	AATGACAGCCTTTTCTGAGAGAGATGATGTTTACACTCTGAAAAATGACGATATGAT	1440	
Db	1594	AATGACAGCCTTTTCTGAGAGAGATGATGTTTACACTCTGAAAAATGACGATATGAT	1653	
Qy	1441	GGATGGAAGAGAAAGATCATGAGGATGAGTGGACAGAGACAGACAGCTCTGTAT	1500	
Db	1654	GGATGGAAGAGAAAGATCATGAGGATGAGTGGACAGAGACAGACAGCTCTGTAT	1713	
Qy	1501	GTTGCGTTCTTACCTGTGATTAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1560	
Db	1714	GTTGCGTTCTTACCTGTGATTAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1773	
Qy	1561	TGTAAAAAAACCTTATTTGCTCGAGAGACCCATATTTGTGATGGAATAAAGAGATGAT	1620	
Db	1774	TGTAAAAAAACCTTATTTGCTCGAGAGACCCATATTTGTGATGGAATAAAGAGATGAT	1833	
Qy	1621	GCCGCGACCATTTATACCCACAGAGACTGACTTTTGGAGAGGATATGAGATGAGC	1680	
Db	1834	GCCGCGACCATTTATACCCACAGAGACTGACTTTTGGAGAGGATATGAGATGAGC	1893	
Qy	1681	AATACAGATGCTGTGGGGAGCTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCAGT	1740	
Db	1894	AATACAGATGCTGTGGGGAGCTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCAGT	1953	
Qy	1741	TCCCTTTTGGCCAGACAAACCATCATGATTCGACGGGCTCAAGAGGGGTATGAGATGAG	1800	
Db	1954	TCCCTTTTGGCCAGACAAACCATCATGATTCGACGGGCTCAAGAGGGGTATGAGATGAG	2013	
Qy	1801	GGAGGAATGCTGGAAGCATCTGCTTGAATCAGCTGACAGCAGACATCCCTTGGGG	1860	
Db	2014	GGAGGAATGCTGGAAGCATCTGCTTGAATCAGCTGACAGCAGACATCCCTTGGGG	2073	
Qy	1861	GCAGTCTTCCCATATATCAACAAAGACAAAGAGAGATGTTGGGAAATTAATCTCAAA	1920	
Db	2074	GCAGTCTTCCCATATATCAACAAAGACAAAGAGAGATGTTGGGAAATTAATCTCAAA	2133	
Qy	1921	GGCCAGACAGCTGTTCCCGTACACCTCTTGGCCATTTGAGATCATCTTGCTTGTGTC	1980	
Db	2134	GGCCAGACAGCTGTTCCCGTACACCTCTTGGCCATTTGAGATCATCTTGCTTGTGTC	2193	
Qy	1981	ATGGGGGGCGTCTTCGCGGCATCACGGTACTGGCGTGTGATCATCGGCGCAAGAC	2040	
Db	2194	ATGGGGGGCGTCTTCGCGGCATCACGGTACTGGCGTGTGATCATCGGCGCAAGAC	2253	
Qy	2041	GTTGCTGTGTGACGAGCAAGAGAGAGAGACTTCACTCGCGCGGGGCTCATGAGC	2100	
Db	2254	GTTGCTGTGTGACGAGCAAGAGAGAGAGACTTCACTCGCGCGGGGCTCATGAGC	2313	
Qy	2101	AGCGTCAACCAAGCTCAGCGGCTCTTTGGGAACTCAATCCAAAGACCCCAAGCGGAG	2160	
Db	2314	AGCGTCAACCAAGCTCAGCGGCTCTTTGGGAACTCAATCCAAAGACCCCAAGCGGAG	2373	
Qy	2161	GCCATCCTCAGGCACTCATGACAAACGAGCACTGCGCACTCCGCGCAACAGGCGCAAG	2220	
Db	2374	GCCATCCTCAGGCACTCATGACAAACGAGCACTGCGCACTCCGCGCAACAGGCGCAAG	2433	
Qy	2221	ATGCTCATTAAGCAGACACGACACCACTGTGAGCTGACGCGCTCTCCCAACCAAGATCA	2280	
Db	2434	ATGCTCATTAAGCAGACACGACACCACTGTGAGCTGACGCGCTCTCCCAACCAAGATCA	2493	
Qy	2281	ACCCCAAGCGTGCAGCAGAGCGGAGACCCAGCGCGGAGCGCGAGTGGAGAGAGAC	2340	
Db	2494	ACCCCAAGCGTGCAGCAGAGCGGAGACCCAGCGCGGAGCGCGAGTGGAGAGAGAC	2553	
Qy	2341	CAGACCTCATCATAGCTGCTCAGCAAAAGAGATGCCCCCATGGGCTCCCTGTGATGCC	2400	
Db	2554	CAGACCTCATCATAGCTGCTCAGCAAAAGAGATGCCCCCATGGGCTCCCTGTGATGCC	2613	
Qy	2401	ACGAGCCTGCCCTGCGGGGCTCCGCCAGCACATCCCGACGCTGTGTGTCCTGCTATC	2460	
Db	2614	ACGAGCCTGCCCTGCGGGGCTCCGCCAGCACATCCCGACGCTGTGTGTCCTGCTATC	2673	
Qy	2461	ACGAGCAGAGGCTTACAGCATGAGTACGTGAGCAGCCCAAAATGAGCGAGTGGCCAG	2520	
Db	2674	ACGAGCAGAGGCTTACAGCATGAGTACGTGAGCAGCCCAAAATGAGCGAGTGGCCAG	2733	
Qy	2521	ATGGCGCTGAGAGACAGGCGCCGACCACTGGAGTATTAAGACATCAAGGAATCTAGC	2580	
Db	2734	ATGGCGCTGAGAGACAGGCGCCGACCACTGGAGTATTAAGACATCAAGGAATCTAGC	2793	
Qy	2581	AGCAAGAGTCCCAACCATGGGTTGAACCTTGGAGAACCTGGACAGCTGCCCCCAAA	2640	
Db	2794	AGCAAGAGTCCCAACCATGGGTTGAACCTTGGAGAACCTGGACAGCTGCCCCCAAA	2853	
Qy	2641	GTTCCACAGGAGGAGGCTCTCCCTGATCCCGGGAGACCTCCCTGTCTCAGACCGGTCTA	2700	
Db	2854	GTTCCACAGGAGGAGGCTCTCCCTGATCCCGGGAGACCTCCCTGTCTCAGACCGGTCTA	2913	
Qy	2701	AGCAAGGCGCTGGAAATGACACTCTCTTCTTCAAGGGGTTGACTATTAAGAGAGCTAC	2760	
Db	2914	AGCAAGGCGCTGGAAATGACACTCTCTTCTTCAAGGGGTTGACTATTAAGAGAGCTAC	2973	
Qy	2761	CCGAGAACTGCTCAGAGAGAGACAGCAGGCGCAC--ACTTCAAAAGAAACAAACACTAA	2819	
Db	2974	CCGAGAACTGCTCAGAGAGAGACAGCAGGCGCAC--ACTTCAAAAGAAACAAACACTAA	3033	
Qy	2820	CTCTCCATTTCTCTC-ACCTGTCCAGAAACCAAGGCTTTGGCAGGGGAGACAAACCGC	2878	
Db	3034	CTCTCCATTTCTCTC-ACCTGTCCAGAAACCAAGGCTTTGGCAGGGGAGACAAACCGC	3093	
Qy	2879	CGCCCGCCCGCAGAGAGGTGAGATCCAGAGGTGACAGAGTCTCCAGCATCTGAGCAG	2938	
Db	3094	CGCCCGCCCGCAGAGAGGTGAGATCCAGAGGTGACAGAGTCTCCAGCATCTGAGCAG	3153	

QY	361	ATTAAAGTCTCTAAAGAAAAACATGATGATGATGTTGTGTGTGGAAACTAAAGCCCTTC	420
Db	610	ATTAAAGTCTCTCTAAAGAAAAACGATGATGATGATGTTGTGTGTGGAACTAAAGCTTTC	669
QY	421	AACCCCTCCGCGAAGAACTATAAGATGATGATGATTTGGAACCAATTGCGGGATGAATTCAGC	480
Db	670	AACCCCTCCGCGAAGAAACATTAAGATGATGATGATTTGGAACCAATTGCGGGATGAATTCAGC	729
QY	481	GGATGGCCAGATGCCCATTTGATGTCCAAAACATGCCAAGCTTGACGTGTGTTGACATGTGA	540
Db	730	GGATGGCCAGATGCCCATTTGATGTCCAAAACATGCCAAGCTTGACGTGTGTTGACATGTGA	789
QY	541	AAACTATACACAGCCAGTGCATGCACTTCCTTGCCATTCAGCAGCACTCATTTACCGAGT	600
Db	790	AAACTATACACAGCCAGTGCATGCACTTCCTTGCCATTCAGCAGCACTCATTTACCGAGT	849
QY	601	CTTGGAAAGACCCCTACCCCTGGGAGACCGTCACAGCCAGATTCAAATAATGTTGAAGAACCA	660
Db	850	CTTGGAAAGACCCCTACCCCTGGGAGACCGTCACAGCCAGATTCAAATAATGTTGAAGAACCA	909
QY	661	TACTTGTGTCAAGCCCGTGGATTAACGGAGATTAATATCACTTCCTCTCCAGGAAATAGCA	720
Db	910	TACTTGTGTCAAGCCCGTGGATTAACGGAGATTAATATCACTTCCTCTCCAGGAAATAGCA	969
QY	721	GTGGAGATTAACACCATAGGAGAAAGATGATTTTCCCAAGATGAGTCAAGTTGTAAAGAT	780
Db	970	GTGGAGATTAACACCATAGGAGAAAGATGATTTTCCCAAGATGAGTCAAGTTGTAAAGAT	1029
QY	781	GATATGGAGAGATCTCAAAGAGTCTCTGGAGAAACATGGACAGTGTCTCGAAGGCGCGC	840
Db	1030	GATATGGAGAGATCTCAAAGAGTCTCTGGAGAAACATGGACAGTGTCTCGAAGGCGCGC	1089
QY	841	TTGAAGTCTAGTTCCTCGAGACCTCATTTTATTTTCAACATTCACAGGCAATTAC	900
Db	1090	TTGAAGTCTAGTTCCTCGAGACCTCATTTTATTTTCAACATTCACAGGCAATTAC	949
QY	901	GATGATTCCTATCAACGSGCGTGTGATGTTGTCTGGCAACGTTTCTACACCTTATAAC	960
Db	1150	GATGATTCCTATCAACGSGCGTGTGATGTTGTCTGGCAACGTTTCTACACCTTATAAC	1209
QY	961	AGCATCCCTGGGTCTGGCAGTCTGTGGCCATGACATGCTGCATTTGGCAGTGTTTTACT	1020
Db	1210	AGCATCCCTGGGTCTGGCAGTCTGTGGCCATGACATGCTGCATTTGGCAGTGTTTTACT	1269
QY	1021	GGGAGATTCAGAGAACAGAGTCTTCCTGATTCACACCTGGACACACATTCCTGATGAACGA	1080
Db	1270	GGGAGATTCAGAGAACAGAGTCTTCCTGATTCACACCTGGACACACATTCCTGATGAACGA	1329
QY	1081	GTTTCCTAAGCCAGGCGCAGGTTGCTGTGTCTGGCTCATCTCTTAAGAAATATGCAACC	1140
Db	1330	GTTTCCTAAGCCAGGCGCAGGTTGCTGTGTCTGGCTCATCTCTTAAGAAATATGCAACC	1389
QY	1141	TCCAAATGATTTCCCTGATGATACCTCTGAACTTCATCAAGACGCAACCGCTCATGATGAG	1200
Db	1390	TCCAAATGATTTCCCTGATGATACCTCTGAACTTCATCAAGACGCAACCGCTCATGATGAG	1449
QY	1201	GCAGTGCCTTCATCTTCAACAGGCCATGATGTTCTCGAAGAACATAGTTCAGATACCGGCTT	1260
Db	1450	GCAGTGCCTTCATCTTCAACAGGCCATGATGTTCTCGAAGAACATAGTTCAGATACCGGCTT	1509
QY	1261	ACCAAAATTCAGATGAGACACAGCTGTGGGCCATATTCGAATACACACTGTGTTTTCTG	1320
Db	1510	ACCAAAATTCAGATGAGACACAGCTGTGGGCCATATTCGAATACACACTGTGTTTTCTG	1569
QY	1321	GGATTCAGAGAGGGAATCATCTTGAAGTTTTTGGCCAGAAATGAAATAGGATGTTTCTA	1380
Db	1570	GGATTCAGAGAGGGAATCATCTTGAAGTTTTTGGCCAGAAATGAAATAGGATGTTTCTA	1629
QY	1381	AATGACAGCCTTTTCTCGAGAGATGATGTTTCAACTCTGAAAAATGCAAGCTATGAT	1440
Db	1630	AATGACAGCCTTTTCTCGAGAGATGATGTTTCAACTCTGAAAAATGCAAGCTATGAT	1689

Query Match 87.2%; Score 2698; DB 11; Length 3333;
 Best Local Similarity 93.9%; Pred. No 0;
 Matches 2907; Conservative 0; Mismatches 21; Indels 167; Gaps 3;

1 ATGAGTCAAGAGCCTTGTCTATATTTTACACATGCTACACTTGTGTGGGGCTGTTTC 60
 214 ATGAGTCAAGAGCCTTGTCTATATTTTACACATGCTACACTTGTGTGGGGCTGTTTC 273
 61 CCAGAGATTTCTGAGCCATACATATTTTGCATGGCACTATACAAAACAGTATCCGGTG 120
 274 CCAGAGATTTCTGAGCCATACATATTTTGCATGGCACTATACAAAACAGTATCCGGTG 333
 121 TTGTGGGCCCAAGAGCCAGAGCAACACACAGAGGAGACAGCCCTGAGATCCAGATG 180
 334 TTGTGGGCCCAAGAGCCAGAGCAACACACAGAGGAGACAGCCCTGAGATCCAGATG 393
 181 ATTATGATTCATGAAGAGGAGCCCTCTACATGCTGCTAGGAGCCATATTATCTGTGAT 240
 394 ATTATGATTCATGAAGAGGAGCCCTCTACATGCTGCTAGGAGCCATATTATCTGTGAT 453
 241 ATAGACATTCACACACAGAGAAATTTATGCAAAAACTGACATGGAAATCTAGA 300
 454 ATAGACATTCACACACAGAGAAATTTATGCAAAAACTGACATGGAAATCTAGA 513
 301 CAGGCCCATGTAGACACATGCAGATGAAGGAAACATAGAGTGAAGTGCACACATTT 360
 514 CAGGCCCATGTAGACACATGCAGATGAAGGAAACATAGAGTGAAGTGCACACATTT 573
 361 ATTAAAGTTCTCTTAAAGAAAGAAACAGATGATGATGTTGTCTGTGGAACATATGCTTC 420
 574 ATTAAAGTTCTCTTAAAGAAAGAAACAGATGATGATGTTGTCTGTGGAACATATGCTTC 633
 421 AACCTTCTCTGAGAAACATATAGATGATGATGATGATGATGATGATGATGATGATGAT 480
 634 AACCTTCTCTGAGAAACATATAGATGATGATGATGATGATGATGATGATGATGATGAT 693
 481 GGAGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
 694 GGAGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 753
 541 AAACATATCTAGGACACAGTACTGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 754 AAACATATCTAGGACACAGTACTGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 813
 601 CTTGAGAGAAAGCCCTACCTGCGGAGCCTCAAGCAGATTTCAAAATGTTGAAGAACCA 660
 814 CTTGAGAGAAAGCCCTACCTGCGGAGCCTCAAGCAGATTTCAAAATGTTGAAGAACCA 873
 661 TACCTTGTTCAGAGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 874 TACCTTGTTCAGAGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 933
 721 GTGAGATATTAACACCATGAGAAAGGTAGTTTCCCAAGAGTGGCTCAGGTTTGTAAAGAT 780
 924 GTGAGATATTAACACCATGAGAAAGGTAGTTTCCCAAGAGTGGCTCAGGTTTGTAAAGAT 993
 781 CATATGAGAGATCTCAAAAGAGTCTGTGAGAAACAGTGAAGTGTCTCTGAAAGCGGC 840
 994 CATATGAGAGATCTCAAAAGAGTCTGTGAGAAACAGTGAAGTGTCTCTGAAAGCGGC 1053
 841 TTGAGTGTCTAGTCTGAGAGCTCTCATTTTATTTCAACATCTCCAGGCACTTACA 900
 1054 TTGAGTGTCTAGTCTGAGAGCTCTCATTTTATTTCAACATCTCCAGGCACTTACA 1113
 901 GATGATATTCGATACAGGGGCGTATGTTGTCTGAGCAAGCTTTTCTACACCTTATTAAC 960
 1114 GATGATATTCGATACAGGGGCGTATGTTGTCTGAGCAAGCTTTTCTACACCTTATTAAC 1173
 961 AGCATTCCTGGGCTGTGCAATCTGTGCTGATGATGATGATGATGATGATGATGATGATGAT 1020
 1174 AGCATTCCTGGGCTGTGCAATCTGTGCTGATGATGATGATGATGATGATGATGATGATGAT 1233

1021 GGGAGATTCAGAGACAGAGAGTCTCTGATTCACCTGAGACACAGTTCCTGATGAGCA 1080
 1234 GGGAGATTCAGAGACAGAGAGTCTCTGATTCACCTGAGACACAGTTCCTGATGAGCA 1293
 1081 GTTCTTACGAGCCAGAGGAGTGTGCTGAGGAGGAGTGTGCTGAGGAGGAGTGTGCTGAG 1140
 1294 GTTCTTACGAGCCAGAGGAGTGTGCTGAGGAGGAGTGTGCTGAGGAGGAGTGTGCTGAG 1353
 1141 TCCATGATGATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
 1354 TCCATGATGATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1413
 1201 GCAAGTCCCTCCATCTTCAACAGAGGAGTGTGCTGAGGAGGAGTGTGCTGAGGAGGAGT 1260
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 1261 ACCAAATTTGAGTGGAGACAGCTGCTGGGAGATATGAGATTCACACTGCTGTTTCTG 1320
 1474 ACCAAATTTGAGTGGAGACAGCTGCTGGGAGATATGAGATTCACACTGCTGTTTCTG 1533
 1321 GGATCAGAGAGGAGATTCATCTGAGGATGATGATGATGATGATGATGATGATGATGATGAT 1380
 1534 GGATCAGAGAGGAGATTCATCTGAGGATGATGATGATGATGATGATGATGATGATGATGAT 1593
 1381 AATGACAGCCTTTTCTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
 1594 AATGACAGCCTTTTCTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1653
 1441 GGATTCAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 1654 GGATTCAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1713
 1501 GTTGGCTTCTTACCTGTGATTAAGTTCCTTGGCGGTGTGAAGCAGATGAGGAAG 1560
 1714 GTTGGCTTCTTACCTGTGATTAAGTTCCTTGGCGGTGTGAAGCAGATGAGGAAG 1773
 1561 TGTAAAAAAGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
 1774 TGTAAAAAAGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1833
 1621 GCGTGCAGCAGATTTTCAACAG 1680
 1834 GCGTGCAGCAGATTTTCAACAG 1893
 1681 AATACAGATGCTGAGGAGAGTGTCAATTCCTTTTGGGACAGTAAATGGGATTCAGAT 1740
 1894 AATACAGATGCTGAGGAGAGTGTCAATTCCTTTTGGGACAGTAAATGGGATTCAGAT 1941
 1741 TCCCTCTTCCAGCAGCAACACATCAGATTCAGAGGAGGAGGATGATGATGATGATGATGAT 1800
 1942 TCCCTCTTCCAGCAGCAACACATCAGATTCAGAGGAGGAGGATGATGATGATGATGATGAT 1941
 1801 GGAGAGATGCTGAGTGAAGCATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1860
 1942 GGAGAGATGCTGAGTGAAGCATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1941
 1861 GCAGTGTCTTCCATTAATTCACAGAGAGAGAGAGATTCGGGAGATTAACCTCAAA 1920
 1942 GCAGTGTCTTCCATTAATTCACAGAGAGAGAGAGATTCGGGAGATTAACCTCAAA 1968
 1921 GGCACAGACACAGTGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
 1969 GGCACAGACACAGTGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2028
 2029 ATGGGAGGCGCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2088
 1981 ATGGGAGGCGCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2040
 2041 GTGGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2100
 2089 GTGGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2148
 2101 AGCGTCACCAAGCTGAGCGGCTCTTTGGGAGACATCAATCCAAAGACCCAAAGCCGAG 2160

Db 2149 AGGTCACCAAGTCTAGCGGCGCTTTGGGAGACATCCAAAGCCAAAGCCGGAG 2208
 QY 2161 GCCATCTCAGCGCACTCATGCAACAAGGCAAGCTCGCCACTCCCGCAACAGGGCAAG 2220
 Db 2209 GCCATCTCAGCGCACTCATGCAACAAGGCAAGCTCGCCACTCCCGCAACAGGGCAAG 2268
 QY 2221 ATGCTATTAAAGCAACCAAGCAACCACTGGAGCTTACAGGCGCTTCCCAACCAAGTCA 2280
 Db 2269 ATGCTATTAAAGCAACCAAGCAACCACTGGAGCTTACAGGCGCTTCCCAACCAAGTCA 2328
 QY 2281 ACCCAAGCGTGGAGAGAGAGAGGCGGAGCCAGCGGGAGAGCGAGTGGAGAGAGAG 2340
 Db 2329 ACCCAAGCGTGGAGAGAGAGAGGCGGAGCCAGCGGGAGAGCGAGTGGAGAGAGAG 2388
 QY 2341 CAGAACCTCATCAATGCTGCAACAAAGGACATGCCCCCAATGGGCTCCCTGTGATTCC 2400
 Db 2389 CAGAACCTCATCAATGCTGCAACAAAGGACATGCCCCCAATGGGCTCCCTGTGATTCC 2448
 QY 2401 AGGAGCTGCGCTTGGGGGCTTCCCGCAGCCACATCCCAAGGCTGGTGGTCCCGCCATC 2460
 Db 2449 AGGAGCTGCGCTTGGGGGCTTCCCGCAGCCACATCCCAAGGCTGGTGGTCCCGCCATC 2508
 QY 2461 AGCAGACAGGCTACACAGCATGATAGTGGACCAAGCCCAATGAAGCGAGTGGCCAG 2520
 Db 2509 AGCAGACAGGCTACACAGCATGATAGTGGACCAAGCCCAATGAAGCGAGTGGCCAG 2568
 QY 2521 ATGGCGCTGAGAGACCAAGGCGCCACACTGGAGTATAGACCATCAAGAACATCTCAGC 2580
 Db 2569 ATGGCGCTGAGAGACCAAGGCGCCACACTGGAGTATAGACCATCAAGAACATCTCAGC 2628
 QY 2581 AGCAAGATGCCCAACATGGGGGAGAACCTTGTGAGAGCACTGGAGCAAGCCGCGCCCAAA 2640
 Db 2629 AGCAAGATGCCCAACATGGGGGAGAACCTTGTGAGAGCACTGGAGCAAGCCGCGCCCAAA 2688
 QY 2641 GTTCCACAGGCGGAGGCGCTCCCTGGGCTCCCGGGAGACCTCCCTGTCTCAGACCGGTCTA 2700
 Db 2689 GTTCCACAGGCGGAGGCGCTCCCTGGGCTCCCGGGAGACCTCCCTGTCTCAGACCGGTCTA 2748
 QY 2701 AGCAAGCGGCTGAGAAATGACACCACTCTTCTTCTAGCGGCTTGCATATAGAGAGCTAC 2760
 Db 2749 AGCAAGCGGCTGAGAAATGACACCACTCTTCTTCTAGCGGCTTGCATATAGAGAGCTAC 2808
 QY 2761 CCCAGCAAGTCCGCAAGAGAGAGCCAGAGCCAGC-ACCTCAAAAAGAAACAACTAA 2819
 Db 2809 CCCAGCAAGTCCGCAAGAGAGAGCCAGAGCCAGCTGACACTCTCTCAAGAAACAACTAA 2868
 QY 2820 CTCTCCCAATTCCTCTC-ACCTCTCCAGAAACAGAGCTTGGCAGGGGAGACAAACCCGC 2878
 Db 2869 CTCTCCCAATTCCTCTC-ACCTCTCCAGAAACAGAGCTTGGCAGGGGAGACAAACCCGC 2928
 QY 2879 CGCCCGCCCGCAGAGGCTGACTTCATCCAGGTGACAGTCTCCAGCCATCTGGCCAGG 2938
 Db 2929 CGCCCGCCCGCAGAGGCTGACTTCATCCAGGTGACAGTCTCCAGCCATCTGGCCAGG 2988
 QY 2939 CCGTACGCTGCTCAGGAGAGCCAGACCTCAAGGCTTCACTCACTGCAAGAGTGGGGC 2998
 Db 2989 CCGTACGCTGCTCAGGAGAGCCAGACCTCAAGGCTTCACTCACTGCAAGAGTGGGGC 3048
 QY 2999 TGAAGCGTACGCTCGCTTAAAGCGGAGCTTACCCCAACCAATCTCTTCTCCCTTT 3058
 Db 3049 TGAAGCGTACGCTCGCTTAAAGCGGAGCTTACCCCAACCAATCTCTTCTCCCTTT 3108
 QY 3059 CCACATCCATGAAGCCCAATGATGCGGTACATTA 3093
 Db 3109 CCACATCCATGAAGCCCAATGATGCGGTACATTA 3143

RESULT 5
 US-09-957-187-5
 ; Sequence 5, Application US/09957187
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 ; GENERAL INFORMATION:

; APPLICANT: Shinkets, Richard A.
 ; APPLICANT: Laroche, William
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
 ; FILE REFERENCE: 15966-540 CIP
 ; CURRENT APPLICATION NUMBER: US/09/957,187
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 ; PRIOR APPLICATION NUMBER: 09/520,781
 ; PRIOR FILING DATE: 2000-03-03
 ; PRIOR APPLICATION NUMBER: 60/234,082
 ; PRIOR FILING DATE: 2000-09-20
 ; PRIOR APPLICATION NUMBER: 60/233,798
 ; PRIOR FILING DATE: 2000-09-19
 ; PRIOR APPLICATION NUMBER: 60/174,485
 ; PRIOR FILING DATE: 2000-01-04
 ; NUMBER OF SEQ ID NOS: 85
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 3333
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (214)..(2865)
 ; NAME/KEY: misc feature
 ; LOCATION: (2882)
 ; OTHER INFORMATION: an n may be any one of a or t or g or c
 US-09-957-187-5
 Query Match 87.2%; Score 2698; DB 11; Length 3333;
 Best Local Similarity 93.9%; Pred. No. 0;
 Matches 2907; Conservative 0; Mismatches 21; Indels 167; Gaps 3;
 QY 1 ATGAGTCAAGAGCGTCTGCTGCTATATTTACACTGCTACACTTGTGGGCGCTTC 60
 Db 214 ATGAGTCAAGAGCGTCTGCTGCTATATTTACACTGCTACACTTGTGGGCGCTTC 273
 QY 61 CCAGAAATTCCTGAGCCATACAGTATTTGCGATGGCACTATACAAACAGTATCCGATG 120
 Db 274 CCAGAAATTCCTGAGCCATACAGTATTTGCGATGGCACTATACAAACAGTATCCGATG 333
 QY 121 TTTGTGGCCACAAGCCAGGAGGAGACCAACAGAGGCAAGGCGTGGATCCAGATG 180
 Db 334 TTTGTGGCCACAAGCCAGGAGGAGACCAACAGAGGCAAGGCGTGGATCCAGATG 393
 QY 181 ATTATGATCATGAAGGAAACCTTACATGCTGCTGAGGACCATATTTATGCTGAT 240
 Db 394 ATTATGATCATGAAGGAAACCTTACATGCTGCTGAGGACCATATTTATGCTGAT 453
 QY 241 ATGAGCAATCACACAGGAGAAATTTATGTAGCAAAAACCTGACATGGAAATCTAGA 300
 Db 454 ATGAGCAATCACACAGGAGAAATTTATGTAGCAAAAACCTGACATGGAAATCTAGA 513
 QY 301 CAGGCGAGTGTAGACACATGCAATGAGAGGAGAAACATAGATGAGTGGCCAACTTT 360
 Db 514 CAGGCGAGTGTAGACACATGCAATGAGAGGAGAAACATAGATGAGTGGCCAACTTT 573
 QY 361 ATTAAGTCTTCTTAAGAAAGAAAGATGATGATGTTGTGCTGCACTAATAGCCTTC 420
 Db 574 ATTAAGTCTTCTTAAGAAAGAAAGATGATGATGTTGTGCTGCACTAATAGCCTTC 633
 QY 421 AACCTTCTCAGAAACTATATAGATGATGATGATGATGATGATGATGATGATGATGAT 480
 Db 634 AACCTTCTCAGAAACTATATAGATGATGATGATGATGATGATGATGATGATGATGAT 693
 QY 481 GGAATGGCAGATGCCATATGATGCCAAACATGCCAAGCTTGGACAGTGTGGAGATGA 540
 Db 694 GGAATGGCAGATGCCATATGATGCCAAACATGCCAAGCTTGGACAGTGTGGAGATGA 753
 QY 541 AAATATATCTAGGACGACGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 Db 754 AAATATATCTAGGACGACGATGATGATGATGATGATGATGATGATGATGATGATGAT 813

QY	601	CTTGAGAAAGCCCTACCCCTGGGAGCGTCACAGCATTCGAAAGAGTGTGAAAGAACCA	660
Db	814	CTTGAGAAAGCCCTACCCCTGGGAGCGTCACAGCATTCGAAAGAGTGTGAAAGAACCA	873
QY	661	TACTTGTTCACCCCGGAGATTACGGAGATTATATCTACTCTCTTCACGGGAAATAGCA	720
Db	874	TACTTGTTCACCCCGGAGATTACGGAGATTATATCTACTCTCTTCACGGGAAATAGCA	933
QY	721	GTCGAGTATACACCATGGGAAAGTAGTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT	780
Db	934	GTCGAGTATACACCATGGGAAAGTAGTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT	993
QY	781	GATATGGAGAGATCTCAAAAGTCTGGGAAACACATGGACGTCGTCCGGAAGGGGCGC	840
Db	994	GATATGGAGAGATCTCAAAAGTCTGGGAAACACATGGACGTCGTCCGGAAGGGGCGC	1053
QY	841	TTGAACCTGCTACCTTCGTGAGACTGTCATTTTATTTCAACATTCCTCCAGGACATTACA	900
Db	1054	TTGAACCTGCTACCTTCGTGAGACTGTCATTTTATTTCAACATTCCTCCAGGACATTACA	1113
QY	901	GATGTGATTGCTATCAACGGGCGTATGTTGTCCGGCAACGTTTTCTACACTTATAC	960
Db	1114	GATGTGATTGCTATCAACGGGCGTATGTTGTCCGGCAACGTTTTCTACACTTATAC	1173
QY	961	AGATCCCTGGGCTGAGTCTGTGCTATGACATGTCATGTCATGTCATGTCATGTCATG	1020
Db	1174	AGATCCCTGGGCTGAGTCTGTGCTATGACATGTCATGTCATGTCATGTCATGTCATG	1233
QY	1021	GGGAGATTCAAGAACGAAAGTCTCTGATTCACCTGAGACACAGTTCCTGATGAACGA	1080
Db	1234	GGGAGATTCAAGAACGAAAGTCTCTGATTCACCTGAGACACAGTTCCTGATGAACGA	1293
QY	1081	GTTCTTAAGCCGACGAGTGTGCTGTGCTGCTCATCTCTCTTAAGAAATATGCAAC	1140
Db	1294	GTTCTTAAGCCGACGAGTGTGCTGTGCTGCTCATCTCTCTTAAGAAATATGCAAC	1353
QY	1141	TTCATGATGTTCCCTGATGATACCTGATCACTCATCAAGACACCCGCTCATGAGATAG	1200
Db	1354	TTCATGATGTTCCCTGATGATACCTGATCACTCATCAAGACACCCGCTCATGAGATAG	1413
QY	1201	GCAGTGCCTCCATCTTCAACAGGCGCATGCTCTCTGAAACAATGTCAGATACCCGCTT	1260
Db	1414	GCAGTGCCTCCATCTTCAACAGGCGCATGCTCTCTGAAACAATGTCAGATACCCGCTT	1473
QY	1261	ACCAAAATGAGGAGACACAGCTGCTGGGCGCATATCAGAAATCACAATGSGGTTTCTG	1320
Db	1474	ACCAAAATGAGGAGACACAGCTGCTGGGCGCATATCAGAAATCACAATGSGGTTTCTG	1533
QY	1321	GGATCAGAGAAAGGAATCATCTTGAAAGTTTTTGGCCAGAAATAGGAATAGTGTGTTCTA	1380
Db	1534	GGATCAGAGAAAGGAATCATCTTGAAAGTTTTTGGCCAGAAATAGGAATAGTGTGTTCTA	1593
QY	1381	AATACAGACCTTTTCTCGAGAGAGATAGTGTTCACAACCTCGAAAAATCGAGTATAGAT	1440
Db	1594	AATACAGACCTTTTCTCGAGAGAGATAGTGTTCACAACCTCGAAAAATCGAGTATAGAT	1653
QY	1441	GGAGTCGAGAACAAAGAGATGAGGAGTGCAGCTGAGACAGAGAACACAGCTCTGTAT	1500
Db	1654	GGAGTCGAGAACAAAGAGATGAGGAGTGCAGCTGAGACAGAGAACACAGCTCTGTAT	1713
QY	1501	GTTTCGTTCTCTACCTGTGTGATTAAGGTTTCCCTTGGCCGGTGTGAACGATGGGAAG	1560
Db	1714	GTTTCGTTCTCTACCTGTGTGATTAAGGTTTCCCTTGGCCGGTGTGAACGATGGGAAG	1773
QY	1561	TGTAAAAAACCCTGTATTTGCTCCAGAGACCCATATTTGATGATGATTAAGAGAGTGTGT	1620
Db	1774	TGTAAAAAACCCTGTATTTGCTCCAGAGACCCATATTTGATGATGATTAAGAGAGTGTGT	1833
QY	1621	GGCGAGACCCATTAATACCCCAACAGACAGATGACTTTTGACAGAGACATAGACGTTGGC	1680
Db	1834	GGCGAGACCCATTAATACCCCAACAGACAGATGACTTTTGACAGAGACATAGACGTTGGC	1893

Db 2809 CCCAGCACTGCTCAGAGAGAGCCACCTGACACCTACTCTCTATCGAAGACACACTTAA 2868
QY 2820 CTCCTCCAAATCTCTCTC-ACCTCTCCAGAAACCGAGACCTTTGGCAGGGGAGACAAACCCG 2878
Db 2869 CCCGACAAATTCACACTCTGACTTTCAAGGGAGACAGACTTTGGGAGGGAGACAAACCCG 2928
QY 2879 CGCCCGCCCGCAGAGGGTGTGACTCTCAATCCAGGTGCACAGTCCAGCCATCTTGCCAGG 2938
Db 2929 CGCCCGCCCGCAGAGGGTGTGACTCTCAATCCAGGTGCACAGTCCAGCCATCTTGCCAGG 2988
QY 2939 CGGTGACGTCTGAGGAGAGCCGACGCTCAACGCTCAACTGACTGACAAAGTCCGGGGC 2998
Db 2989 CCGTACTGTCTGAGGAGAGCCGACGCTCAACGCTCAACTGACTGACAAAGTCCGGGGC 3048
QY 2999 TGAAGCGTACGCGCTCTGCTAAAGCCGAGACGTACCCCAACCATCCCTTTGCTCCCTTT 3058
Db 3049 TGAAGCGTACGCGCTCTGCTAAAGCCGAGACGTACCCCAACCATCCCTTTGCTCCCTTT 3108
QY 3059 CCACATCATGTAAGCCCAATGATGCTGTTACATTA 3093
Db 3109 CCACATCATGTAAGCCCAATGATGCTGTTACATTA 3143

RESULT 6

US-09-991-053-29
Sequence 29, Application US/09991053
Publication No. US20030003532A1
GENERAL INFORMATION:
APPLICANT: Shinkets, Richard A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES ENCODING HUMAN SLIT-
FILE REFERENCE: 15966-540 CON 5-10
CURRENT APPLICATION NUMBER: US/09/991,053
PRIOR FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: USSN 60/123,667
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: 09/520,781
PRIOR FILING DATE: 2000-03-08
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 29
LENGTH: 1890
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1890)
US-09-991-053-29

Query Match 60.88: Score 1881.6; DB 11: Length 1890;

Best Local Similarity 99.88; Freq. No. 0;

Matches 1884: Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 49 GGGGCTGGTTCCTCCAGAAATCTGAGCCATCAATGATTTGTCATGGAATATACAAA 108
Db 1 GGATCCGGTTTCCAGAAATCTGAGCCATCAATGATTTGTCATGGAATATACAAA 60
QY 109 CAGTATCCGTTGTTGTGGGCCACAGCCAGGACGAAACACACACAGAGGACAGGCTG 168
Db 61 CAGTATCCGTTGTTGTGGGCCACAGCCAGGACGAAACACACACAGAGGACAGGCTG 120
QY 169 GACATCCGATGATTAATGATGATGAAGGAAACCTCTACATTTGCTGAGGAGCAATAT 228
Db 121 GACATCCGATGATTAATGATGATGAAGGAAACCTCTACATTTGCTGAGGAGCAATAT 180
QY 229 TATATCTGTATATAGACACATCAACAGGAAATTTATTTAGCAAAAAAAGTACA 288
Db 181 TATATCTGTATATAGACACATCAACAGGAAATTTATTTAGCAAAAAAAGTACA 240
QY 289 TGAATATAGACAGCCGAGGTAGACACATGCAAGATGAAGGAAAAATTAAGATAG 348
Db 241 TGAATATAGACAGCCGAGGTAGACACATGCAAGATGAAGGAAAAATTAAGATAG 300

QY 349 TGGCACAATTTATTAAGTTCTTCTAAAGAAAAACATGATGATTTGTCTGTGA 408
Db 301 TGGCACAATTTATTAAGTTCTTCTAAAGAAAAACATGATGATTTGTCTGTGA 360
QY 409 ACTATGCTTCAACCCCTCTCTGAGAAACATTAAGATGATGATGGAACATTTGGG 468
Db 361 ACTATGCTTCAACCCCTCTCTGAGAAACATTAAGATGATGATGGAACATTTGGG 420
QY 469 GATGAATTCAGCGGAATGGCCAGATGGCCATATGATGCAACATGCAAGCTTGACATG 528
Db 421 GATGAATTCAGCGGAATGGCCAGATGGCCATATGATGCAACATGCAAGCTTGACATG 480
QY 529 TTTGCAATGGAATTAATTAATCTGACGCAAGATGATGATTTCTTGTGATGAGCATG 588
Db 481 TTTGCAATGGAATTAATTAATCTGACGCAAGATGATGATTTCTTGTGATGAGCATG 540
QY 589 ATTATCCGGAATCTTGAAGAAAGCCATACCTGGGGAGCCGCAAGCAATGCAAAATG 648
Db 541 ATTATCCGGAATCTTGAAGAAAGCCATACCTGGGGAGCCGCAAGCAATGCAAAATG 600
QY 649 TTGAAGAACCATCTTTGTTCAAGCCGTGATTAAGAGATTAATCTACTTCTCTC 708
Db 601 TTGAAGAACCATCTTTGTTCAAGCCGTGATTAAGAGATTAATCTACTTCTCTC 660
QY 709 AGGGAATAGCAGTGGAGTATTAACACCATGAGGAAAGTATGTTTCCAGAGTGGCTAG 768
Db 661 AGGGAATAGCAGTGGAGTATTAACACCATGAGGAAAGTATGTTTCCAGAGTGGCTAG 720
QY 769 GTTGTAGATGATGATGAGGAGATTCGAAGATCTCTGAGAAACATGAGCGCTG 828
Db 721 GTTGTAGATGATGATGAGGAGATTCGAAGATCTCTGAGAAACATGAGCGCTG 780
QY 829 CTGAAGCGCGCTTGAAGTGTGCAAGTCTGGAAGTCTCATTTTATTTCAACATCTC 888
Db 781 CTGAAGCGCGCTTGAAGTGTGCAAGTCTGGAAGTCTCATTTTATTTCAACATCTC 840
QY 889 CAGGCAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 948
Db 841 CAGGCAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
QY 949 ACACCTTATTAACACATCTCTGAGTGTGCAAGTCTGGAAGTCTCATTTTATTTCAACATCTC 1008
Db 901 ACACCTTATTAACACATCTCTGAGTGTGCAAGTCTGGAAGTCTCATTTTATTTCAACATCTC 960
QY 1009 AGTGTTTTACTGGAATTTAAGGACAGAGTCTCTGATTTCCACCTGAGACACAGTT 1068
Db 961 AGTGTTTTACTGGAATTTAAGGACAGAGTCTCTGATTTCCACCTGAGACACAGTT 1020
QY 1069 CCTGATGAGAGTCTCTGAGTGTGCAAGTCTGGAAGTCTCATTTTATTTCAACATCTC 1128
Db 1021 CCTGATGAGAGTCTCTGAGTGTGCAAGTCTGGAAGTCTCATTTTATTTCAACATCTC 1080
QY 1129 AGATATGCAACCTCCATGATGATGATGATGATGATGATGATGATGATGATGATG 1188
Db 1081 AGATATGCAACCTCCATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
QY 1189 CTGATGATGAGGAGTGTGCAAGTCTCTGAGTGTGCAAGTCTCATTTTATTTCAACATCTC 1248
Db 1141 CTGATGATGAGGAGTGTGCAAGTCTCTGAGTGTGCAAGTCTCATTTTATTTCAACATCTC 1200
QY 1249 AGATACGCTCTTACCAAAATTTCAAGTGAACAGCTGTGAGGCAATATCAATCACT 1308
Db 1201 AGATACGCTCTTACCAAAATTTCAAGTGAACAGCTGTGAGGCAATATCAATCACT 1260
QY 1309 GTGCTTTTCTGGAATGAGAAAGGAAATCTTTGAGTTTGGCCAGAAATAGAAAT 1368
Db 1261 GTGCTTTTCTGGAATGAGAAAGGAAATCTTTGAGTTTGGCCAGAAATAGAAAT 1320
QY 1369 AGTGTTTTCTAATATGACAGCTTTCTGAGGAGATGAGATGATTTACACTCTGAAAA 1428
Db 1321 AGTGTTTTCTAATATGACAGCTTTCTGAGGAGATGAGATGATTTACACTCTGAAAA 1380


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Db 1081 AGATATGCAACCTCCATGAGTCCCTGATGATACCTGAACTTCAATCAAGACGACCG 1140
QY 1189 CTCTGATGATGAGGAGGCGCTCCATCTTCAACGAGGCGATGTTCTTGAGAACATGTC 1248
Db 1141 CTCTGATGATGAGGAGGCGCTCCATCTTCAACGAGGCGATGTTCTTGAGAACATGTC 1200
QY 1249 AGATACCGGCTTACCAAAATTCAGTGGACACAGCTGCTGGCCCATATCAGATCAGACT 1308
Db 1201 AGATACCGGCTTACCAAAATTCAGTGGACACAGCTGCTGGCCCATATCAGATCAGACT 1260
QY 1309 GTGGTTTTCTGGGATGAGAGAGGGAATCATCTGTAAGTTTTTGGCCCAATATGAAAT 1368
Db 1261 GTGGTTTTCTGGGATGAGAGAGGGAATCATCTGTAAGTTTTTGGCCCAATATGAAAT 1320
QY 1369 AGTGGTTTTCTAAATGACAGCCCTTCTCTGAGAGATGAGTGTTCACACTGGAATAA 1428
Db 1321 AGTGGTTTTCTAAATGACAGCCCTTCTCTGAGAGATGAGTGTTCACACTGGAATAA 1380
QY 1429 TGCAGCTATGATGAGTGAAGACAAAAGATCATGSGGATGAGCTGAGACAGCAAGC 1488
Db 1381 TGCAGCTATGATGAGTGAAGACAAAAGATCATGSGGATGAGCTGAGACAGCAAGC 1440
QY 1489 AGCTCTGCTATGTTGGCTCTCTACCTGTGTATAGTAAAGTTCCTTGGCCGCTGGA 1548
Db 1441 AGCTCTGCTATGTTGGCTCTCTACCTGTGTATAGTAAAGTTCCTTGGCCGCTGGA 1500
QY 1549 CGACATGGAAGTGTAAATAAACTGTATTGCTCTCAGAGACCCATATTGTGATGATA 1608
Db 1501 CGACATGGAAGTGTAAATAAACTGTATTGCTCTCAGAGACCCATATTGTGATGATA 1560
QY 1609 AAGGAAGGTGTGCTCTGACGATTTATCAACCCACAGACAGCTGTTTGGACAGAGC 1668
Db 1561 AAGGAAGGTGTGCTCTGACGATTTATCAACCCACAGACAGCTGTTTGGACAGAGC 1620
QY 1669 ATAGAGGTGCAATACAGATGCTGTGGGAGCTGTACAAATTCCTTGTGGACCTAAAT 1728
Db 1621 ATAGAGGTGCAATACAGATGCTGTGGGAGCTGTACAAATTCCTTGTGGACCTAAAT 1680
QY 1729 GGGCATTCAGTCCCTCTCTGCGCAGACAAACCATATCATTTGAGGCGCTCAAGAGGG 1788
Db 1681 GGGCATTCAGTCCCTCTCTGCGCAGACAAACCATATCATTTGAGGCGCTCAAGAGGG 1740
QY 1789 TATGAGCTAGGAGAGATGCTGAGCTGGAAGCATGTGCTGACTCACTGACAGACA 1848
Db 1741 TATGAGCTAGGAGAGATGCTGAGCTGGAAGCATGTGCTGACTCACTGACAGACA 1800
QY 1849 GACCCCTTGGGGAGTGTCTTCCATATATCACAAGACAAGAAAGGAGTTCGGGAA 1908
Db 1801 GACCCCTTGGGGAGTGTCTTCCATATATCACAAGACAAGAAAGGAGTTCGGGAA 1860
QY 1909 AGTTACCTCAAGGCGCAGACAGCTGG 1936
Db 1861 AGTTACCTCAAGGCGCAGACAGCTGG 1888

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RESULT 8

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US-09-957-187-82
; Sequence 82, Application US/09957187
; Publication No. US2003005451A1
; GENERAL INFORMATION:
; APPLICANT: Shinketsu, Richard A.
; APPLICANT: Larochelle, William
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
; FID REFERENCE: 15966-540 CIP
; CURRENT FILING DATE: US/09/957,187
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20

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; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 1890
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1884)
US-09-957-187-82

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Query Match 60.8%; Score 1881.6; DB 11; Length 1890;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1884; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 49 GGGGCTGTTTCCAGAAATCTGAGCCAAATCAGTATTTGGCATGGCACTATACAAA 108
Db 1 GGATCCGGTTCACAGAGATTCGACCCAAATGATTTTCATGCGACTATACAAA 60
QY 109 CAGTATCCGGTGTGTTGGGCGACAGAGCGAGAAACACACAGAGGACAGGCTG 168
Db 61 CAGTATCCGGTGTGTTGGGCGACAGAGCGAGAAACACACAGAGGACAGGCTG 120
QY 169 GACATCCAGATGATTAATGATCAGACAGAAACCTCTACATTCCTGCTAGGACCATTT 228
Db 121 GACATCCAGATGATTAATGATCAGACAGAAACCTCTACATTCCTGCTAGGACCATTT 180
QY 229 TATACGTGTGATATAGACACATTCACACAGGAGAAATTTTGTAGCAAAAACAGCA 288
Db 181 TATACGTGTGATATAGACACATTCACACAGGAGAAATTTTGTAGCAAAAACAGCA 240
QY 289 TGGAAATCTAGACAGGCGGATGTAGACACATGACGAATGAAGGAGAAACATTAAGATGAG 348
Db 241 TGGAAATCTAGACAGGCGGATGTAGACACATGACGAATGAAGGAGAAACATTAAGATGAG 300
QY 349 TGGCAACAATTTAATAAGTCTCTAAGAAACGATGTATGATTTGTCTGTGA 408
Db 301 TGGCAACAATTTAATAAGTCTCTAAGAAACGATGTATGATTTGTCTGTGA 360
QY 409 ACTAATGCTTCAACCCCTTCTCTGAGAAACTATAAGATGATATGATTTGAACCATTCGGG 468
Db 361 ACTAATGCTTCAACCCCTTCTCTGAGAAACTATAAGATGATATGATTTGAACCATTCGGG 420
QY 469 GATGAATTCAGCGGATGCGCAGATGCCATATGATGGCAAAACATGCCAAGGTTGCACTG 528
Db 421 GATGAATTCAGCGGATGCGCAGATGCCATATGATGGCAAAACATGCCAAGGTTGCACTG 480
QY 529 TTTGAGATGGAATACTTACTCAAGCCAGTGAATGATCTTCTTGCATTGACGACATC 588
Db 481 TTTGAGATGGAATACTTACTCAAGCCAGTGAATGATCTTCTTGCATTGACGACATC 540
QY 589 ATTTACCGAGTCTTTGAGAAAGCCCTACCTCGCGACCGTCACAGCAGATTTCAAAATGG 648
Db 541 ATTTACCGAGTCTTTGAGAAAGCCCTACCTCGCGACCGTCACAGCAGATTTCAAAATGG 600
QY 649 TTGAAGAACAATCTTTGTCACAGCGGTGATTTAGAGATTAATATCTACTTCTTCTC 708
Db 601 TTGAAGAACAATCTTTGTCACAGCGGTGATTTAGAGATTAATATCTACTTCTTCTC 660
QY 709 AGGAAATAGCAGTGGAGTATACCAATGGAAGAGTAGTTTCCCAAGAGTGGCTCAG 768
Db 661 AGGAAATAGCAGTGGAGTATACCAATGGAAGAGTAGTTTCCCAAGAGTGGCTCAG 720
QY 769 GTTTTAAGATGATATGAGAGATCTCAAAAGAGCTCGAGAAACAGTGGAGCTGTC 828
Db 721 GTTTTAAGATGATATGAGAGATCTCAAAAGAGCTCGAGAAACAGTGGAGCTGTC 780
QY 829 CTGAAGGCGCGTAACTGCTCAGTTCCTGAGAGCTCATTTTATTTCAACATCTC 888

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Sequence 60, Application US/09925299
Patent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 60
LENGTH: 1472
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (129)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (130)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-60
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Query Match 18.3%; Score 565; DB 9; Length 1472;

Best Local Similarity 99.5%; Pred. No. 3,4e-166;

Matches 576; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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QY 2515 GCCCAGATGGCGCTGGAGGACCCGCGCCACACTGAGTAAAGACCATCAGAACAT 2514
DB 13 GCCCAGATGGCGCTGGAGGACCCGCGCCACACTGAGTAAAGACCATCAGAACAT 72
QY 2575 CTCGACGACGAAGATGCCAACCATGGGGTGAACCTTGAGAACTGGACAGCCTGCC 2634
DB 73 CTCGACGACGAAGATGCCAACCATGGGGTGAACCTTGAGAACTGGACAGCCTNNCC 132
QY 2635 CCCAAGTTCACAGCGGAGGAGGCTCCCTGGGTCGCCCGGAGAGCTCCCTGTCAGACC 2694
DB 133 CCCAAGTTCACAGCGGAGGAGGCTCCCTGGGTCGCCCGGAGAGCTCCCTGTCAGACC 192
QY 2695 GGTCTAAGCAAGCGGCTGGAAATGACACACTCTCTCTACGAGGGTGTATAGAGG 2754
DB 193 GGTCTAAGCAAGCGGCTGGAAATGACACACTCTCTCTACGAGGGTGTATAGAGG 252
QY 2755 AGTACCCCAAGAACTGCTACGAGAGGACCCAGGCACTCTCAAAAGAAACAC 2814
DB 253 AGTACCCCAAGAACTGCTACGAGAGGACCCAGGCACTCTCAAAAGAAACAC 311
QY 2815 ACTAAGCTCCCAATTCCTCTCACCTCTCCAGAAACAGAGCTTTGGCAGGGAGACAC 2874
DB 312 ACTAAGCTCCCAATTCCTCTCACCTCTCCAGAAACAGAGCTTTGGCAGGGAGACAC 371
QY 2875 CCGCGCGCGCGCGCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCGAGCTTGGC 2934
DB 372 CCGCGCGCGCGCGCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCGAGCTTGGC 431
QY 2935 CAGGCGGTGACTGTCTCGAGGACGCCAGCTTCAACGCTTACAACTCACTGACAGGTG 2994
DB 432 CAGGCGGTGACTGTCTCGAGGACGCCAGCTTCAACGCTTACAACTCACTGACAGGTG 491
QY 2995 GGGCTGAAGCGGTACGCCCTGCTAAAGCGGAGGTACCCCCCAACCATCTTTGCTCC 3054
DB 492 GGGCTGAAGCGGTACGCCCTGCTAAAGCGGAGGTACCCCCCAACCATCTTTGCTCC 551
QY 3055 CTTTCCATCCATGAAGCCCAATGATGCGTACATTA 3093
DB 552 CTTTCCATCCATGAAGCCCAATGATGCGTACATTA 590
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RESULT 11

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US-09-925-299-60
Sequence 60, Application US/09925299
Publication No. US20030040617A9
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 60
LENGTH: 1472
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (129)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (130)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-60
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Query Match 18.3%; Score 565; DB 11; Length 1472;

Best Local Similarity 99.5%; Pred. No. 3,4e-166;

Matches 576; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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QY 2515 GCCCAGATGGCGCTGGAGGACCCGCGCCACACTGAGTAAAGACCATCAGAACAT 2514
DB 13 GCCCAGATGGCGCTGGAGGACCCGCGCCACACTGAGTAAAGACCATCAGAACAT 72
QY 2575 CTCGACGACGAAGATGCCAACCATGGGGTGAACCTTGAGAACTGGACAGCCTGCC 2634
DB 73 CTCGACGACGAAGATGCCAACCATGGGGTGAACCTTGAGAACTGGACAGCCTNNCC 132
QY 2635 CCCAAGTTCACAGCGGAGGAGGCTCCCTGGGTCGCCCGGAGAGCTCCCTGTCAGACC 2694
DB 133 CCCAAGTTCACAGCGGAGGAGGCTCCCTGGGTCGCCCGGAGAGCTCCCTGTCAGACC 192
QY 2695 GGTCTAAGCAAGCGGCTGGAAATGACACACTCTCTCTACGAGGGTGTATAGAGG 2754
DB 193 GGTCTAAGCAAGCGGCTGGAAATGACACACTCTCTCTACGAGGGTGTATAGAGG 252
QY 2755 AGTACCCCAAGAACTGCTACGAGAGGACCCAGGCACTCTCAAAAGAAACAC 2814
DB 253 AGTACCCCAAGAACTGCTACGAGAGGACCCAGGCACTCTCAAAAGAAACAC 311
QY 2815 ACTAAGCTCCCAATTCCTCTCACCTCTCCAGAAACAGAGCTTTGGCAGGGAGACAC 2874
DB 312 ACTAAGCTCCCAATTCCTCTCACCTCTCCAGAAACAGAGCTTTGGCAGGGAGACAC 371
QY 2875 CCGCGCGCGCGCGCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCGAGCTTGGC 2934
DB 372 CCGCGCGCGCGCGCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCGAGCTTGGC 431
QY 2935 CAGGCGGTGACTGTCTCGAGGACGCCAGCTTCAACGCTTACAACTCACTGACAGGTG 2994
DB 432 CAGGCGGTGACTGTCTCGAGGACGCCAGCTTCAACGCTTACAACTCACTGACAGGTG 491
QY 2995 GGGCTGAAGCGGTACGCCCTGCTAAAGCGGAGGTACCCCCCAACCATCTTTGCTCC 3054
DB 492 GGGCTGAAGCGGTACGCCCTGCTAAAGCGGAGGTACCCCCCAACCATCTTTGCTCC 551
QY 3055 CTTTCCATCCATGAAGCCCAATGATGCGTACATTA 3093
DB 552 CTTTCCATCCATGAAGCCCAATGATGCGTACATTA 590
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RESULT 12
US-10-391-413-3
: Sequence 3, Application US/10391413
: Publication No. US20030167482A1
: GENERAL INFORMATION:
: APPLICANT: KIMURA, Toru et al.
: TITLE OF INVENTION: NOVEL SEMAPHORIN 2 AND GENE ENCODING THE SAME
: FILE REFERENCE: 0020-5120P
: CURRENT APPLICATION NUMBER: US/10/391,413
: CURRENT FILING DATE: 2003-03-19
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 3
: LENGTH: 3524
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: 5'UTR
: LOCATION: (1)..(38)
: OTHER INFORMATION:
: FEATURE:
: NAME/KEY: 3'UTR
: LOCATION: (2706)..(3524)
: OTHER INFORMATION:
: NAME/KEY: CDS
: LOCATION: (39)..(2702)
: OTHER INFORMATION:
US-10-391-413-3

Query Match 18.0%; Score 555.4; DB 12; Length 3524;
Best Local Similarity 60.0%; Pred. No. 6,5e-163;
Matches 1026; Conservative 0; Mismatches 656; Indels 27; Gaps 5;

QY 13 GCCTTGGCTATATTTACACCTGCTACACTGCTGGGCGTGGTTTCCAGAAATTC 72
DB 72 GCCCTGCTGCTTCTGCTGCTACTGCGGGGGCCGACGCCCTTCTCGAAGACCG 131
QY 73 GAGCAATCAATATTTGGCAGTGGCACTATACAAAAGATCCGGGTGTTTGGCCAC 132
DB 132 CCGCGCTTACGCTGCGGCCCGGAGGACTACCTGAAACCTATCCCGTGTGTTGGGAGC 191
QY 133 AAGCAGAGGAGGAAACACAC-----ACAGAGGACAGGCGTGCATCCAGATGATATG 186
DB 192 GGGCGCGGAGCGCTGACCGCCCGGAGAGGTGCTGACACCTCAACATCCAGCGAGTCTG 251
QY 187 ATCATGAACGGAACCTCTACATGCTGCTGAGGACCAATATTACTGTTGATATAGAC 246
DB 252 CGGCTCAACAGGAGCGTGTTCATGATGGGAGGAGGACAACTCTACCGCTAGAGCTGGAG 311
QY 247 ACATCACACACGAGAGAAATTTATTAGCAAAAAGTGCATGGAATCTAGACAGGCC 306
DB 312 CCCCCACGTCACAGGAGCTGCGGTACACAGAGAGTGAATGAGATCTTAACCCGAC 371
QY 307 GATGTAGACACATGACAGATGAGAGGAAACATTAAGATGATGCCAATTTATTAA 366
DB 372 GACATTAACGCTGTGAGATGAGAGGCAACAGAGGCGGAGTGTCCGAATTTGTAAG 431
QY 367 GTTCTTCTAAGAAAAGATGATGATGTTGTTGCTGCTGAGACTAAATGCTTACCT 426
DB 432 GTGCTGCTCTCTCGGAGAGTCCACGCTTGTGTGCGGTTCCAAAGCCTTACACCG 491
QY 427 TCCGCAAGAAATCTAAGATGATGATGATGATGATGATGATGATGATGATGATG 486
DB 492 GTGTGCGGCACTACAGATGACACCTGAGCGCTCGAGGACCAATATAGCGGTATG 551
QY 487 GCCAGATGCCCATATGATGATGATGATGATGATGATGATGATGATGATGATG 546
DB 552 GCCCGCTGCGGATGAGAGCCCAAGCAGCGCAATGTTGCCCTTCTGAGAGGATGTC 611
QY 547 TACTGAGCAGAGTACTGACTTCTGTTGCTGATGAGCAGTATTTACCGAGTCTTGA 606
DB 612 TTCACAGCTACTGTTACGAGCTTCTAGCATGATGATGATGATGATGATGATGATG 671

QY 607 GAAGCCCTACCTGCGGAGCGCTGACAGCATTCATAAATGTTGAAAGAACCATCTT 666
DB 672 GACAGCGCCACCTGCGGACCGCTGAACATGATCTCAGATGTTCAAAAGACCTTACTT 731
QY 667 GTTCAGCCCGTGTAGATGAGATTTATCTACTTCTCTCCAGGAAATAGCAGTGAG 726
DB 732 GTCCATCGGCTGAGAGTGGGAGGACGATGCTACTTCTCTCCGAGATTCGATGGAG 791
QY 727 TATACACCATGAGAAAGTATGTTTCCCAAGAGTGCCTAGTTTGTGAATATGATG 786
DB 792 TTTACTACTCTGAGAAAGTGTGATGTCGCGGCGGACCGAGTGTGCAACAGACGTG 851
QY 787 GGAGGATCTCAAAAGTCTGAGAAAGTGTGAGAGTGTGCTCCAGAGCGCGCTGAGC 846
DB 852 GGAGGCTCCCGCCGCTGCTGAGAGAGTGTGAGAGTGTGCTCCAGAGCGCGCTGAGC 911
QY 847 TGCATGTTCCGAGAGTCTGATTTTATTTATTTATTTATTTATTTATTTATTTATTT 906
DB 912 TGTCTGTACCCGAGAGTCTCCATTTTCTACTTCAACGCTGCTGAGAGTGTGAGAGT 971
QY 907 ATTGATCAACAGGAGCGTATGTTGCTGAGCAACGTTTCTACACCTTATACAGCATC 966
DB 972 GTACAGCTCGGGGCGCGCGCGCTGATGCTGAGCGGCTTTCACGCGCAGACAGCATC 1031
QY 967 CCGGCTGTGAGTGTGCTGCTATGATGATGATGATGATGATGATGATGATGATGATG 1026
DB 1032 CCGGCTGTGAGTGTGCTGCTATGATGATGATGATGATGATGATGATGATGATGATG 1091
QY 1027 TTCAAGGAAACAGAGTCTCCGATTCACCTGACACACAGTCTGATGAGAGATTCCT 1086
DB 1092 TTCCGAGAGCAGAGTCTCCCGAGTCTGAGAGCGCGGAGAGATCAGTGTCT 1151
QY 1087 AAGCCAGGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1146
DB 1152 CGAGCCCGCGCGGCTGCT-----GGGCAACCCCGCGGATGAGCATGATGCTCCAGC 1205
QY 1147 GAGTTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1206
DB 1206 GCTTGTGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1265
QY 1207 CCTTCATCTTCAACAGGCGCATGCTGCTGAGAAACATGTCAGATACCGGCTTACCAA 1266
DB 1266 CCTTCGCTGAGGCGCATGAGCGCGCTGAGATCTGAGAGACCTGATGAGGACACAGCTG 1325
QY 1267 ATTGCACTGAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1326
DB 1326 GTGCTGTGAGAGTGTGAGAGCGCGCGCGCTGAGGCAACAGACGCTGCTGCTGCTGCT 1385
QY 1327 GAGAAGGAAATCATCTGAGATTTT-----GGGCAAGATAGAAATAGGTTTCTA 1380
DB 1386 GAGCGGAGGAGCGGCTCTCAATTTCTGCTCGGCGCCATGCGCAGACCTCAGAGAGCT 1445
QY 1381 AATGACACCTTTCTGAGAGAGATGATGATTTTCAACTCTGAATAATGAG-----C 1434
DB 1446 GGGCTCAGTGTCTCTGAGAGATTTGAGACCTACCGCGGAGAGTGTGAGAGCGCC 1505
QY 1435 TATGATGAGTGTGAGAGAAAGATGATGAGGATGAGGATGAGGATGAGGATGAGGAT 1494
DB 1506 GCGCGTGTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1565
QY 1495 CTGATGATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1554
DB 1566 CTGCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1625
QY 1555 GGAAGTGTAAAAAACCCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1614
DB 1626 TCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1685
QY 1615 GGTGCTGCTGAGACCATTTATCAOCCCAACAGAGAGTACTGTTGACAGAGCATAGAG 1674
DB 1686 GGGT-----CTGATCTTCTCAGAGCGGAGCAGAGCGCGCTTTGAGCAGAGAGTGTCT 1742

QY 73 GAGCCATAGATATTCGATGCGCACTATACAAACAGTATCCGGTGTGTGGGCCAC 132
 112 CCGCGCTTAGCGGTGGGCCCGAGGAGTACTGAAACACTATCCGGTGTGTGGGCCAGC 171
 QY 133 AAGCCAGAGGAGCAACAC-----ACAGAGGACAGGCTGACATCCGAGATGATG 186
 172 GGGCCCGGAGCGCTGAGCCCGGAGAGGCTGAGAGCTCAACATCCAGAGCTCTG 231
 QY 187 ATCATGAGAGGAGCCCTCATATGCTGAGGAGACATATTTATAGTGTGATAGAC 246
 232 CGGCTCAACAGAGAGCTGTTACTTGGGAGAGGAGACACTTACCGCTAGAGCTGAG 291
 QY 247 ACATCACACAGAGAGAAATTTATGTAGCAAAAACTGACATGAAATCTAGACAGCC 306
 292 CCCCCCAGTCCAGGAGGTGCGGTACAGAGAGAGCTGACCTGGAGATCTTAACCCAGC 351
 QY 307 GATGTAGACATGACAAATGAGAGGAGAAACATAGAGTAGGCCCACTTATATAA 366
 352 GACATAAAGCTGTGTGATGAAAGGCAAAAGGAGGCGAGGTGTCGAAACTTCTGTAAG 411
 QY 367 GTTCTTTAAGAAAAAGATGATGATGATGTTGTGTGTGAAACTATGCTTCAACCT 426
 412 GTGTGTCTTGGGAGAGAGTCCAGCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 471
 QY 427 TCCGCAAGAACTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 486
 472 GT 531
 QY 487 GCCAGATGCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 546
 532 GCCGCTGT 591
 QY 547 TACTAGCAAGTACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 606
 592 TTTACAGTACTGTTTACAGTACTGTTTACAGTACTGTTTACAGTACTGTTTACAGT 651
 QY 607 GAAAGCCCTACCTGCGAGAGAGTCAAGAGAGTCAAGAGTCAAGAGTCAAGAGTCAAG 666
 652 GACAGGCCACCTGCGAGAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGT 711
 QY 667 GTTCAGGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 726
 712 GTTCATGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 771
 QY 727 TATAACACCATGAGAGAGTATGTTTCCCAAGAGTGTGCTGAGTTTGTAGATGATG 786
 772 TTTAATTAACCTGAGAGAGTGTGTTGCTGCGGTGCGGTGCGGTGCGGTGCGGTG 831
 QY 787 GGAGAGTCTCAAAAGTCTGAGAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAG 846
 832 GGAAGGCTCCCGCGGTGAGAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAG 891
 QY 847 TGCTAGTCTGAGAGTCTGATTTTATTTTCAACATTTCCAGGAGTATACAGATG 906
 892 TGCTGTGAGAGAGTCTGATTTTCAACATTTCCAGGAGTATACAGAGTCTG 951
 QY 907 ATTCGATCAAGGAGT 966
 952 GTCAAGCTTGGGAGGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1011
 QY 967 CCGGAGTCTGAGAGTCTGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 1026
 1012 CCGGAGTCTGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1071
 QY 1027 TTTCAAGAGAGAGTCTGATTTTCAACATTTCCAGGAGTATACAGATGATG 1086
 1072 TTTCAAGAGAGAGTCTGATTTTCAACATTTCCAGGAGTATACAGATGATG 1131
 QY 1087 AAGCCAGAGAGT 1146
 1132 CGAGCCCGCGGT 1185
 QY 1147 GAGTTCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1206

Db 1186 GCGTGTGAGAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1245
 QY 1207 CCGTCACTTTCAACAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1266
 1246 CCGTCACTTTCAACAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1305
 QY 1267 ATTGAGTGTGAGAGT 1326
 1306 GTGCTGTGTGAGAGT 1365
 QY 1327 GAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
 1366 GAGGCGGAGAGT 1425
 QY 1381 AATGACAGCTTTTCTGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1434
 1426 GCGTCACTTTTCTGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1485
 QY 1435 TATGATGAGTGTGAG 1494
 1486 GCGGCTGTGAG 1545
 1495 CTGTATGAGT 1554
 QY 1546 CTGTATGAGT 1605
 1555 GCGAGTGTGAG 1614
 1606 TCGGAGTGTGAG 1665
 QY 1615 GGT 1674
 1666 GCGT-----CTGTATGAGT 1722
 QY 1675 GGT 1703
 1723 GGGGCGAG 1751
 Db 1751 GGGGCGAG

RESULT 14
 US-10-035-977-34
 : Sequence 34, Application US/10035977
 : Publication No. US20030134327A1
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Desnoyers, Luc
 : APPLICANT: Eaton, Dan L.
 : APPLICANT: Goddard, Audrey
 : APPLICANT: Godowski, Paul J.
 : APPLICANT: Gurney, Austin L.
 : APPLICANT: Pap, James
 : APPLICANT: Stewart, Timothy A.
 : APPLICANT: Watanabe, Colin K.
 : APPLICANT: Wood, William I.
 : APPLICANT: Zhang, Zemin
 :
 : TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 : FILE REFERENCE: P303081C10
 :
 : CURRENT APPLICATION NUMBER: US/10/035,977
 :
 : PRIORITY FILING DATE: 2001-12-26
 :
 : PRIOR APPLICATION NUMBER: 60/085579
 :
 : PRIOR FILING DATE: 1998-05-15
 :
 : PRIOR APPLICATION NUMBER: 60/112514
 :
 : PRIOR FILING DATE: 1998-12-15
 :
 : PRIOR APPLICATION NUMBER: 60/113300
 :
 : PRIOR FILING DATE: 1998-12-22
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 : PRIOR APPLICATION NUMBER: 60/113430
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 : PRIOR FILING DATE: 1998-12-23
 :
 : PRIOR APPLICATION NUMBER: 60/113605
 :
 : PRIOR FILING DATE: 1998-12-23
 :
 : PRIOR APPLICATION NUMBER: 60/113621
 :
 : PRIOR FILING DATE: 1998-12-23
 :
 : PRIOR APPLICATION NUMBER: 60/114140

